

| Result No. | Score | Query |      | Length | DB        | ID        | Description        |
|------------|-------|-------|------|--------|-----------|-----------|--------------------|
|            |       | Match | %    |        |           |           |                    |
| 1          | 2282  | 100.0 | 2282 | 6      | AR043313  | Sequence  | AR043313 Sequence  |
| 2          | 2282  | 100.0 | 2282 | 6      | AR067737  | Sequence  | AR067737 Sequence  |
| 3          | 2282  | 100.0 | 2282 | 6      | I56851    | Sequence  | I56851 Sequence    |
| 4          | 2282  | 100.0 | 2282 | 6      | AR224830  | Sequence  | AR224830 Sequence  |
| 5          | 2282  | 100.0 | 2282 | 6      | AR403899  | Sequence  | AR403899 Sequence  |
| 6          | 2282  | 100.0 | 2282 | 6      | AR429415  | Sequence  | AR429415 Sequence  |
| 7          | 2269  | 99.4  | 2269 | 6      | AR176322  | Sequence  | AR176322 Sequence  |
| 8          | 2269  | 99.4  | 2269 | 6      | BD271280  | Compositi | BD271280 Compositi |
| 9          | 2269  | 99.4  | 2269 | 6      | BD273390  | Cancer tr | BD273390 Cancer tr |
| 10         | 2269  | 99.4  | 2269 | 6      | AR183468  | Sequence  | AR183468 Sequence  |
| 11         | 2269  | 99.4  | 2269 | 6      | AR183517  | Sequence  | AR183517 Sequence  |
| 12         | 2269  | 99.4  | 2269 | 6      | AR1213705 | Sequence  | AR1213705 Sequence |
| 13         | 2269  | 99.4  | 2269 | 6      | AR217276  | Sequence  | AR217276 Sequence  |
| 14         | 2269  | 99.4  | 2269 | 6      | AR282748  | Sequence  | AR282748 Sequence  |
| 15         | 2269  | 99.4  | 2269 | 6      | AR451799  | Sequence  | AR451799 Sequence  |
| 16         | 2269  | 99.4  | 2269 | 6      | AR482244  | Sequence  | AR482244 Sequence  |
| 17         | 2269  | 99.4  | 2269 | 6      | AX042263  | Sequence  | AX042263 Sequence  |
| 18         | 2269  | 99.4  | 2269 | 6      | AX490657  | Sequence  | AX490657 Sequence  |
| 19         | 2269  | 99.4  | 2269 | 6      | AX671082  | Sequence  | AX671082 Sequence  |

|    |      |  |      |
|----|------|--|------|
| Db | 241  | ACGACCCAGCCATGGCAGCGTAGCAGCCCTGCGTTCACAGCGCAGCAGCTCGGACTC        | 300  |
| Qy | 301  | TGGA CGTGTGTTGCCCTCAAGTTTGCTAAAGTCTGCTGTTTATTACTGGAAGAAGAAATGT   | 360  |
| Db | 301  | TGGACGTGTGTTTGCCCTCAAGTTTGCTAAAGTGTCTGTTTATTACTGGAAGAAGAAATGT    | 360  |
| Qy | 361  | GGCAGATGTGTTCTTTACTCTGAGCTGTGATCTTGCTTTGGCCGAGCCTATAACAACCT      | 420  |
| Db | 361  | GGCAGATGTGTTCTTTACTCTGAGCTGTGATCTTGCTTTGGCCGAGCCTATAACAACCT      | 420  |
| Qy | 421  | TTCGGAAGAGCATGCACAGCATAGAAAGAAAGCAATATCAGGCTCCAGCATGGGCTCTGCA    | 480  |
| Db | 421  | TTCGGAAGAGCATGCACAGCATAGAAAGAAAGCAATATCAGGCTCCAGCATGGGCTCTGCA    | 480  |
| Qy | 481  | GCTACACTTTCTCTCCAGAGATGGAACAACTGTCGCGCTCTTCTCCAGCCCTACGTGT       | 540  |
| Db | 481  | GCTACACTTTCTCTCCAGAGATGGAACAACTGTCGCGCTCTTCTCCAGCCCTACGTGT       | 540  |
| Qy | 541  | CCAAATGCTGTGCAGAGGAGCGCGCGCTCGAATACGATGACTCGGTGCAGAGCGTCGAAG     | 600  |
| Db | 541  | CCAAATGCTGTGCAGAGGAGCGCGCGCTCGAATACGATGACTCGGTGCAGAGCGTCGAAG     | 600  |
| Qy | 601  | TGCTGGAGAAACATCATCGAAAAACAACACTCAGTGGCTTAATGAAGCTTGAGAAATTATATCC | 660  |
| Db | 601  | TGCTGGAGAAACATCATCGAAAAACAACACTCAGTGGCTTAATGAAGCTTGAGAAATTATATCC | 660  |
| Qy | 661  | AGGACACATCAAGAAGAAATGTTAGAGATACAGCAGAAATGCAGTACAGAAACCGACGG      | 720  |
| Db | 661  | AGGACACATCAAGAAGAAATGTTAGAGATACAGCAGAAATGCAGTACAGAAACCGACGG      | 720  |
| Qy | 721  | CTGTGATGATAGAAATAGGACAAACCTGTTGAAACAAACAGCTGAGCAAAACCGGAAAT      | 780  |
| Db | 721  | CTGTGATGATAGAAATAGGACAAACCTGTTGAAACAAACAGCTGAGCAAAACCGGAAAT      | 780  |
| Qy | 781  | TAACTGATGTGAAGCCCAAGTATTAATCAGACCAGACACTTGAACTTCAGCTCTTGG        | 840  |
| Db | 781  | TAACTGATGTGAAGCCCAAGTATTAATCAGACCAGACACTTGAACTTCAGCTCTTGG        | 840  |
| Qy | 841  | AACACTCCCTCTCGACAAAAAATAATTGGAAAAACAGATTTTGGACCAAGCCAGTGAAATAA   | 900  |
| Db | 841  | AACACTCCCTCTCGACAAAAAATAATTGGAAAAACAGATTTTGGACCAAGCCAGTGAAATAA   | 900  |
| Qy | 901  | ACAAATTCGAAGATAGAAACAGTTTCTAGAAAAGAGGTGTAGCTATCGAAGACAAGC        | 960  |
| Db | 901  | ACAAATTCGAAGATAGAAACAGTTTCTAGAAAAGAGGTGTAGCTATCGAAGACAAGC        | 960  |
| Qy | 961  | ACATCATCAACTACGTCAATAAAAGAGAGAAAGATCAGCTACAGGTGTAGTATCCA         | 1020 |
| Db | 961  | ACATCATCAACTACGTCAATAAAAGAGAGAAAGATCAGCTACAGGTGTAGTATCCA         | 1020 |
| Qy | 1021 | AGCAAAATTCATCATTTGAAGAACTAGAAAAAAAATAGTGCTGCCACCGTGCAATAAT       | 1080 |
| Db | 1021 | AGCAAAATTCATCATTTGAAGAACTAGAAAAAAAATAGTGCTGCCACCGTGCAATAAT       | 1080 |
| Qy | 1081 | CAGTTCTTCAANAGCAGCAATGATCTCATGGAGCAGTTAATACTTACTGACTATGA         | 1140 |
| Db | 1081 | CAGTTCTTCAANAGCAGCAATGATCTCATGGAGCAGTTAATACTTACTGACTATGA         | 1140 |
| Qy | 1141 | TGTCACATCAAACTCAGCTAAGGACCCCACTGTTGCTAAAGAAAGAAACAATCAGTTCA      | 1200 |
| Db | 1141 | TGTCACATCAAACTCAGCTAAGGACCCCACTGTTGCTAAAGAAAGAAACAATCAGTTCA      | 1200 |
| Qy | 1201 | GAGACTGTGTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTCA CGTTTAACAT      | 1260 |
| Db | 1201 | GAGACTGTGTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTCA CGTTTAACAT      | 1260 |
| Qy | 1261 | TCCCTAAATCTTACAGAAGAGATCAAGGCCCTACTGTGACATGGAAGCTTGGAGGAGCGGGT   | 1320 |
| Db | 1261 | TCCCTAAATCTTACAGAAGAGATCAAGGCCCTACTGTGACATGGAAGCTTGGAGGAGCGGGT   | 1320 |
| Qy | 1321 | GGA CAATTTATTCAGCGA CGTGAGGATGGCAGCGTTGATTTTTCAGAGCACTTGAAAAAAT  | 1380 |
| Db | 1321 | GGA CAATTTATTCAGCGA CGTGAGGATGGCAGCGTTGATTTTTCAGAGCACTTGAAAAAAT  | 1380 |

|            |                                    |   |                 |
|------------|------------------------------------|---|-----------------|
| Qy         | 1381                               | ATAAAGTGGGATTTGGTAAACCTTTCAGGAGAAATATTGGCTGGGAAATGAGTTTGTTCGC   | 1440            |
| Db         | 1381                               | ATAAAGTGGGATTTGGTAAACCTTTCAGGAGAAATATTGGCTGGGAAATGAGTTTGTTCGC   | 1440            |
| Qy         | 1441                               | AACGTACTAATCAGCAACGCTATGCTCTTAAANAATACACCTTAAAGACTGGGAAGGGAATG  | 1500            |
| Db         | 1441                               | AACGTACTAATCAGCAACGCTATGCTCTTAAANAATACACCTTAAAGACTGGGAAGGGAATG  | 1500            |
| Qy         | 1501                               | AGGCTTACTCATTTGATGAACATTTCTCTCTCAAGTGAAGAACTCAATATTAGGATTC      | 1560            |
| Db         | 1501                               | AGGCTTACTCATTTGATGAACATTTCTCTCTCAAGTGAAGAACTCAATATTAGGATTC      | 1560            |
| Qy         | 1561                               | ACCTTAAAGGACTTACAGGACAGCCGGCAAAATAGCAGCATCAGCCACACGGAATG        | 1620            |
| Db         | 1561                               | ACCTTAAAGGACTTACAGGACAGCCGGCAAAATAGCAGCATCAGCCACACGGAATG        | 1620            |
| Qy         | 1621                               | ATTTTAAAGCAAAAGGATGGAGACAAACGACAAATATGTTTGCAAATGTTTCACAAATGCTAA | 1680            |
| Db         | 1621                               | ATTTTAAAGCAAAAGGATGGAGACAAACGACAAATATGTTTGCAAATGTTTCACAAATGCTAA | 1680            |
| Qy         | 1681                               | CAGGAGGCTGGTGGTTGATGCATGTGGTCTTCCAACTTGAAACGAAATGTAATATCCAC     | 1740            |
| Db         | 1681                               | CAGGAGGCTGGTGGTTGATGCATGTGGTCTTCCAACTTGAAACGAAATGTAATATCCAC     | 1740            |
| Qy         | 1741                               | AGAGGCAGAAACAAATAAGTTTCAACGGCATTAATATGGTACTACTGGAAGGCTCAGGCT    | 1800            |
| Db         | 1741                               | AGAGGCAGAAACAAATAAGTTTCAACGGCATTAATATGGTACTACTGGAAGGCTCAGGCT    | 1800            |
| Qy         | 1801                               | ATTTCGCTCAAGGCCAACCAATGATGATCCGACAGAGATTTCTTAAACATCCAGTCCA      | 1860            |
| Db         | 1801                               | ATTTCGCTCAAGGCCAACCAATGATGATCCGACAGAGATTTCTTAAACATCCAGTCCA      | 1860            |
| Qy         | 1861                               | CCTGAGGAATGCTCGAACTATTTTCAAGACTTAAGCCAGTGCACCTGAAAGTCAACGG      | 1920            |
| Db         | 1861                               | CCTGAGGAATGCTCGAACTATTTTCAAGACTTAAGCCAGTGCACCTGAAAGTCAACGG      | 1920            |
| Qy         | 1921                               | CTGCGCACTGTGTCTCTTCCACACAGAGGGCGTGTGCTCGGTGCTGACGGGACCCACA      | 1980            |
| Db         | 1921                               | CTGCGCACTGTGTCTCTTCCACACAGAGGGCGTGTGCTCGGTGCTGACGGGACCCACA      | 1980            |
| Qy         | 1981                               | TGCTCAGATTAGAGCCTGTAACTTTATCATTAACTTGCACTTAACTTAAACGGACCAA      | 2040            |
| Db         | 1981                               | TGCTCAGATTAGAGCCTGTAACTTTATCATTAACTTAACTTAAACGGACCAA            | 2040            |
| Qy         | 2041                               | GCAAGACCCCTAAACATCCATATTTGTGATTAGACAGAACACCTATGCAAGATGAACCCG    | 2100            |
| Db         | 2041                               | GCAAGACCCCTAAACATCCATATTTGTGATTAGACAGAACACCTATGCAAGATGAACCCG    | 2100            |
| Qy         | 2101                               | AGGCTGAGAAATCAGACTGACAGTTTACAGACGCTGCTGTCAACCAAGAAATGTTATGTG    | 2160            |
| Db         | 2101                               | AGGCTGAGAAATCAGACTGACAGTTTACAGACGCTGCTGTCAACCAAGAAATGTTATGTG    | 2160            |
| Qy         | 2161                               | CAAGTTTATCAGTAAATAACTGGAACCAAGAACACATTATGTTATACAAATACAGATCATCT  | 2220            |
| Db         | 2161                               | CAAGTTTATCAGTAAATAACTGGAACCAAGAACACATTATGTTATACAAATACAGATCATCT  | 2220            |
| Qy         | 2221                               | TGGAATGCAATCTTCTGAGCACTGTTTATACACTGTGTAAATAACCAATATGTCCTGAAT    | 2280            |
| Db         | 2221                               | TGGAATGCAATCTTCTGAGCACTGTTTATACACTGTGTAAATAACCAATATGTCCTGAAT    | 2280            |
| Qy         | 2281                               | TC 2282   |                 |
| Db         | 2281                               | TC 2282   |                 |
| RESULT 2   |                                    |   |                 |
| AR067737   |                                    |   |                 |
| LOCUS      | AR067737                           | 2282 bp   | DNA             |
| DEFINITION | Sequence 5 from patent US 5851797. | linear  | PAT 29-SEP-1999 |
| ACCESSION  | AR067737                           |   |                 |
| VERSION    | AR067737.1                         | GI:5998959  |                 |
| KEYWORDS   |                                    |   |                 |

RESULT 2  
AR067737  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS



|                                    |      |  |                                     |      |  |
|------------------------------------|------|--|-------------------------------------|------|--|
| Db                                 | 1921 | CTGCGCATTGTGTCTCTCTTCCACCA                 | CAGAGGCGGTGTGCTCGGTGCTGACGGGACCCACA | 1980 |  |
| Qy                                 | 1981 | TGCTCCAGATTAGAGCTGTAAACTTTTATCACTTAAAC     | CTTGATCACTTAAACGGACCCAAA            | 2040 |  |
| Db                                 | 1981 | TGCTCCAGATTAGAGCTGTAAACTTTTATCACTTAAAC     | CTTGATCACTTAAACGGACCCAAA            | 2040 |  |
| Qy                                 | 2041 | GCAAGACCCCTAAACATCCATAATTTGTGATTAGACAGAC   | CACCTATGCAAGATGAACCCG               | 2100 |  |
| Db                                 | 2041 | GCAAGACCCCTAAACATCCATAATTTGTGATTAGACAGAC   | CACCTATGCAAGATGAACCCG               | 2100 |  |
| Qy                                 | 2101 | AGGCTGAGAAATCAGACTGACAGCTTTACAGACCTGCTG    | TACAAACAAGATGTTATGTG                | 2160 |  |
| Db                                 | 2101 | AGGCTGAGAAATCAGACTGACAGCTTTACAGACCTGCTG    | TACAAACAAGATGTTATGTG                | 2160 |  |
| Qy                                 | 2161 | CAAAGTTTATCAGTAATAACTCGAAAAACAGAACACT      | TTATGTTATACAATACAGATCATCT           | 2220 |  |
| Db                                 | 2161 | CAAAGTTTATCAGTAATAACTCGAAAAACAGAACACT      | TTATGTTATACAATACAGATCATCT           | 2220 |  |
| Qy                                 | 2221 | TGGAACCTGCATTCTTCTGAGCACTGTTTATACACTGT     | GTGTAAATACCCATATGCTCTGAAT           | 2280 |  |
| Db                                 | 2221 | TGGAACCTGCATTCTTCTGAGCACTGTTTATACACTGT     | GTGTAAATACCCATATGCTCTGAAT           | 2280 |  |
| Qy                                 | 2281 | TC 2282                                    |                                     |      |  |
| Db                                 | 2281 | TC 2282                                    |                                     |      |  |
| RESULT 3                           |      |  |                                     |      |  |
| 156851                             |      |  |                                     |      |  |
| LOCUS                              |      |  |                                     |      |  |
| DEFINITION                         |      |  |                                     |      |  |
| ACCESSION                          |      |  |                                     |      |  |
| VERSION                            |      |  |                                     |      |  |
| KEYWORDS                           |      |  |                                     |      |  |
| SOURCE                             |      |  |                                     |      |  |
| ORGANISM                           |      |  |                                     |      |  |
| REFERENCE                          |      |  |                                     |      |  |
| AUTHORS                            |      |  |                                     |      |  |
| TITLE                              |      |  |                                     |      |  |
| JOURNAL                            |      |  |                                     |      |  |
| FEATURES                           |      |  |                                     |      |  |
| source                             |      |  |                                     |      |  |
| 1. :2282                           |      |  |                                     |      |  |
| /organism="unknown"                |      |  |                                     |      |  |
| /mol_type="unassigned DNA"         |      |  |                                     |      |  |
| ORIGIN                             |      |  |                                     |      |  |
| Query Match                        |      |  |                                     |      |  |
| Best Local Similarity              |      |  |                                     |      |  |
| Matches 2282; Conservative         |      |  |                                     |      |  |
| 0; Mismatches 0; Indels 0; Gaps 0; |      |  |                                     |      |  |
| Qy                                 | 1    | GAATTCTCTGGGTGGTGTATCTCTCCAGCCTTGAGGGAGGAA | CAACACTGTAGGA                       | 60   |  |
| Db                                 | 1    | GAATTCTCTGGGTGGTGTATCTCTCCAGCCTTGAGGGAGGAA | CAACACTGTAGGA                       | 60   |  |
| Qy                                 | 61   | TCCTGGGAGAGAGGAAACAAAGGACCGTGAAGCTCTCTGT   | AAAAAGCTGACACAGCCCTC                | 120  |  |
| Db                                 | 61   | TCCTGGGAGAGAGGAAACAAAGGACCGTGAAGCTCTCTGT   | AAAAAGCTGACACAGCCCTC                | 120  |  |
| Qy                                 | 121  | CCAAGTGAGCAGGACTGTGTTCTTCCCACTGCAATCTGAC   | AGTTTACTGCAATGCTGGAGAG              | 180  |  |
| Db                                 | 121  | CCAAGTGAGCAGGACTGTGTTCTTCCCACTGCAATCTGAC   | AGTTTACTGCAATGCTGGAGAG              | 180  |  |
| Qy                                 | 181  | ACACAGCAGTAAACCAAGGTTTCTCTAGTGAAGGAGGAA    | GAGAGAGCTTTTCATTG                   | 240  |  |
| Db                                 | 181  | ACACAGCAGTAAACCAAGGTTTCTCTAGTGAAGGAGGAA    | GAGAGAGCTTTTCATTG                   | 240  |  |
| Qy                                 | 241  | ACGGACCCAGCCATGGCAGCGTAGCAGCCCTCGGTTT      | CAGACGGCAGCAGCTCGGGA                | 300  |  |
| Db                                 | 241  | ACGGACCCAGCCATGGCAGCGTAGCAGCCCTCGGTTT      | CAGACGGCAGCAGCTCGGGA                | 300  |  |
| Qy                                 | 301  | TGGACGTGTGTTTGGCCCTCAAGTTTGCTAAGCTGCTGG    | TGTTATTACTGAAGAAAGAAATGT            | 360  |  |

|    |      |   |                             |      |  |
|----|------|---|-----------------------------|------|--|
| Db | 301  | TGGACGTGTGTTTGGCCCTCAAGTTTGCTAAGCTGCTGG | TGTTATTACTGAAGAAAGAAATGT    | 360  |  |
| Qy | 361  | GGCAGATTGTTTCTTTACTCTGAGCTGTGATCTTGTCT  | TGTGGCCGCGCAGCCTATAACAAC    | 420  |  |
| Db | 361  | GGCAGATTGTTTCTTTACTCTGAGCTGTGATCTTGTCT  | TGTGGCCGCGCAGCCTATAACAAC    | 420  |  |
| Qy | 421  | TTCCGGAAGAGCATGAGCAGCATAGGAAAGAGCAATAT  | CAGGTCAGCATGGGTCCTGCA       | 480  |  |
| Db | 421  | TTCCGGAAGAGCATGAGCAGCATAGGAAAGAGCAATAT  | CAGGTCAGCATGGGTCCTGCA       | 480  |  |
| Qy | 481  | GCTACACTTTCTCTCTCCAGAGATGGAACAAC        | TGCGCTCTTCTCCAGCCCTTACGTTG  | 540  |  |
| Db | 481  | GCTACACTTTCTCTCTCCAGAGATGGAACAAC        | TGCGCTCTTCTCCAGCCCTTACGTTG  | 540  |  |
| Qy | 541  | CCAAATGCTGTGAGAGGACCGCGCTCGAATACGAT     | GACTCGGTGCAGAGGCTGCAG       | 600  |  |
| Db | 541  | CCAAATGCTGTGAGAGGACCGCGCTCGAATACGAT     | GACTCGGTGCAGAGGCTGCAG       | 600  |  |
| Qy | 601  | TGCTGGAGAACATCATGTGAAACCAACACTCAGT      | TGGCTTAATGAAGCTTGAGAA       | 660  |  |
| Db | 601  | TGCTGGAGAACATCATGTGAAACCAACACTCAGT      | TGGCTTAATGAAGCTTGAGAA       | 660  |  |
| Qy | 661  | AGGACAAATGGAAGAAATGTTAGAGATACAGCA       | AGATTCAGTACAGAACCCAGCG      | 720  |  |
| Db | 661  | AGGACAAATGGAAGAAATGTTAGAGATACAGCA       | AGATTCAGTACAGAACCCAGCG      | 720  |  |
| Qy | 721  | CTGTGATGATAGAAATAGGACAAACCTGTTGAA       | CCAAACAGCTGAGCAACCGGAGT     | 780  |  |
| Db | 721  | CTGTGATGATAGAAATAGGACAAACCTGTTGAA       | CCAAACAGCTGAGCAACCGGAGT     | 780  |  |
| Qy | 781  | TAACTGATGTGGAAGCCCAAGTATTAAATCAG        | ACCAAGCTTGAACCTTCACTCTTGG   | 840  |  |
| Db | 781  | TAACTGATGTGGAAGCCCAAGTATTAAATCAG        | ACCAAGCTTGAACCTTCACTCTTGG   | 840  |  |
| Qy | 841  | AACACTCCCTCTCGACAAACAAATTTGAAAA         | ACAGATTTTGGACCAAGCTGAAATAA  | 900  |  |
| Db | 841  | AACACTCCCTCTCGACAAACAAATTTGAAAA         | ACAGATTTTGGACCAAGCTGAAATAA  | 900  |  |
| Qy | 901  | ACAAATTCAGAGATAGAAACAGTTTCTTAG          | AAAAAGAGTGTAGCTATGGAAGCA    | 960  |  |
| Db | 901  | ACAAATTCAGAGATAGAAACAGTTTCTTAG          | AAAAAGAGTGTAGCTATGGAAGCA    | 960  |  |
| Qy | 961  | ACATCATCCAACTACAGTCAATATAAAGAA          | AGAAAGATCAGCTACAGTGTAGTATCA | 1020 |  |
| Db | 961  | ACATCATCCAACTACAGTCAATATAAAGAA          | AGAAAGATCAGCTACAGTGTAGTATCA | 1020 |  |
| Qy | 1021 | AGCAAAATTCATCAATTTGAAGAACTAG            | AAAAAATAGTACCTGCCAGCTGAA    | 1080 |  |
| Db | 1021 | AGCAAAATTCATCAATTTGAAGAACTAG            | AAAAAATAGTACCTGCCAGCTGAA    | 1080 |  |
| Qy | 1081 | CAGTTCTTCAAAAGCAGCAACATGATCTCAT         | GAGACAGTTAACTTACTGACTATGA   | 1140 |  |
| Db | 1081 | CAGTTCTTCAAAAGCAGCAACATGATCTCAT         | GAGACAGTTAACTTACTGACTATGA   | 1140 |  |
| Qy | 1141 | TGTCCACATCAAACTCAGCTAAGGACCCCACT        | GTGTTGCTTAAAGAGAAACAAATC    | 1200 |  |
| Db | 1141 | TGTCCACATCAAACTCAGCTAAGGACCCCACT        | GTGTTGCTTAAAGAGAAACAAATC    | 1200 |  |
| Qy | 1201 | GAGACTGTGCTGAAGTATTTCAANTCAGG           | ACACCAAAATGGCATCTACAGTTAA   | 1260 |  |
| Db | 1201 | GAGACTGTGCTGAAGTATTTCAANTCAGG           | ACACCAAAATGGCATCTACAGTTAA   | 1260 |  |
| Qy | 1261 | TCCCTTAATTTACAGAGAGATCAAGGCT            | TACTGTGACATGGAAGCTGGAGG     | 1320 |  |
| Db | 1261 | TCCCTTAATTTACAGAGAGATCAAGGCT            | TACTGTGACATGGAAGCTGGAGG     | 1320 |  |
| Qy | 1321 | GGACAAATTTATCAGCAGCTGAGGATG             | CAGGTTGATTTTTCAGAGGACTT     | 1380 |  |
| Db | 1321 | GGACAAATTTATCAGCAGCTGAGGATG             | CAGGTTGATTTTTCAGAGGACTT     | 1380 |  |
| Qy | 1381 | ATTAAGTGGGATTTGGTAAACCTTTCAG            | GAGAAATTTGGCTGGAAATCAGTT    | 1440 |  |
| Db | 1381 | ATTAAGTGGGATTTGGTAAACCTTTCAG            | GAGAAATTTGGCTGGAAATCAGTT    | 1440 |  |



|    |      |  |      |
|----|------|--|------|
| Db | 1381 | ATAAAGTGGGATTTGGTAACCCCTTACGGAGAAATATTGGCTGGGAAATAGATTTGTTTCGC | 1440 |
| Qy | 1441 | AACTGACTAATCAGCAACGCTATGTCTGTTAAATAATACACCTTAAAGACTGGGAAGGAATG | 1500 |
| Db | 1441 | AACTGACTAATCAGCAACGCTATGTCTGTTAAATAATACACCTTAAAGACTGGGAAGGAATG | 1500 |
| Qy | 1501 | AGGCTTACTCATTGTATGAAATCTTCTCAAGTGAAGAACTCAATATATAGATTTC        | 1560 |
| Db | 1501 | AGGCTTACTCATTGTATGAAATCTTCTCAAGTGAAGAACTCAATATATAGATTTC        | 1560 |
| Qy | 1561 | ACCTTAAAGCACTTACAGGACACGCGGCAAAATAGACGATCAGCAACACGAGGAATG      | 1620 |
| Db | 1561 | ACCTTAAAGCACTTACAGGACACGCGGCAAAATAGACGATCAGCAACACGAGGAATG      | 1620 |
| Qy | 1621 | ATTTTAGCACAAAGGATGGAGACAAACGACAAATATTTTCCAAATGTTTCAAAATGCTAA   | 1680 |
| Db | 1621 | ATTTTAGCACAAAGGATGGAGACAAACGACAAATATTTTCCAAATGTTTCAAAATGCTAA   | 1680 |
| Qy | 1681 | CAGGAGCTGGTGGTGTGATGCAATGTGGTCTTCCAACTTGAACGGGAATGTAATATCCAC   | 1740 |
| Db | 1681 | CAGGAGCTGGTGGTGTGATGCAATGTGGTCTTCCAACTTGAACGGGAATGTAATATCCAC   | 1740 |
| Qy | 1741 | AGAGGACGAAACAAATTAAGTTCAACGGCAATTAATGGTACTACTGGAAGGCTCAGGCT    | 1800 |
| Db | 1741 | AGAGGACGAAACAAATTAAGTTCAACGGCAATTAATGGTACTACTGGAAGGCTCAGGCT    | 1800 |
| Qy | 1801 | ATTTCGCTCAAGGCGCACAAACATGATGATCCGACGAGATTTCTTAAACATCCAGTCCA    | 1860 |
| Db | 1801 | ATTTCGCTCAAGGCGCACAAACATGATGATCCGACGAGATTTCTTAAACATCCAGTCCA    | 1860 |
| Qy | 1861 | CCTGAGGAACGTCTCGAACTATTTTCAAGAATTAAAGCCAGTGCACTGAAAGTCAAGG     | 1920 |
| Db | 1861 | CCTGAGGAACGTCTCGAACTATTTTCAAGAATTAAAGCCAGTGCACTGAAAGTCAAGG     | 1920 |
| Qy | 1921 | CTGGCACTGTGCTCTTCCACACAGAGGGGTGTGCTGGTGTGAGCGGACCCACA          | 1980 |
| Db | 1921 | CTGGCACTGTGCTCTTCCACACAGAGGGGTGTGCTGGTGTGAGCGGACCCACA          | 1980 |
| Qy | 1981 | TGCTCCAGATTAGAGCTGTAACTTTTATCACTTAAACTTTGCACTCACTTAAACGACCAAA  | 2040 |
| Db | 1981 | TGCTCCAGATTAGAGCTGTAACTTTTATCACTTAAACTTTGCACTCACTTAAACGACCAAA  | 2040 |
| Qy | 2041 | GCAAGACCTTAAACATCCATAATTTGTGATTAGACAGAACACCTTATGCAAAAGATGAACCG | 2100 |
| Db | 2041 | GCAAGACCTTAAACATCCATAATTTGTGATTAGACAGAACACCTTATGCAAAAGATGAACCG | 2100 |
| Qy | 2101 | AGGCTGAGATCAGACTGACAGTTTACAGAGCTGTGTACACCAAGAAATGTTATGTG       | 2160 |
| Db | 2101 | AGGCTGAGATCAGACTGACAGTTTACAGAGCTGTGTACACCAAGAAATGTTATGTG       | 2160 |
| Qy | 2161 | CAAGTTTATCAGTAAATAACTGGAAACAGAACACTTTATGTTATACAAATACAGATCATCT  | 2220 |
| Db | 2161 | CAAGTTTATCAGTAAATAACTGGAAACAGAACACTTTATGTTATACAAATACAGATCATCT  | 2220 |
| Qy | 2221 | TGGAACCTGCACTTCTTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGCTCTGAAT | 2280 |
| Db | 2221 | TGGAACCTGCACTTCTTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGCTCTGAAT | 2280 |
| Qy | 2281 | TC 2282  |      |
| Db | 2281 | TC 2282  |      |

RESULT 4  
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LOCUS  
DEFINITION Sequence 5 from patent US 6441137.  
ACCESSION AR224830  
VERSION AR224830.1 GI:23333863  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

|                            |   |   |
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| REFERENCE                  | 1 (bases 1 to 2282)   |   |
| AUTHORS                    | Davis, S. and Vancopoulos, G.D.                             |   |
| TITLE                      | Expressed ligand-vascular intercellular signalling molecule |   |
| JOURNAL                    | Patent: US 6441137-A 5 27-AUG-2002;                         |   |
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| Best Local Similarity      | 100.0%; Pred. No. 0;  |   |
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| Db                         | 1   | GAATTCCTGGTGGTGTATATCTCTCCAGCCTTTGAGGGAGGGAACAACACTGTAGGA 60        |
| Qy                         | 61  | TCGGGGAGAGAGAACAAAGGACCGTGAAAGCTGCTCTGTAAAGCTGACACAGCCCTC 120       |
| Db                         | 61  | TCGGGGAGAGAGAACAAAGGACCGTGAAAGCTGCTCTGTAAAGCTGACACAGCCCTC 120       |
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| Db                         | 181   | AACACAGCAGTAAAAAACAGGTTTGTCTTGGAAAAAGAGAAAGAAAGAAAGAAAGAAAG 240     |
| Qy                         | 241   | ACGGACCCAGCCATGGCAGGCTAGCAGCCCTGCGTTTCAGACGGCAGCAGCTGGGACTC 300     |
| Db                         | 241   | ACGGACCCAGCCATGGCAGGCTAGCAGCCCTGCGTTTCAGACGGCAGCAGCTGGGACTC 300     |
| Qy                         | 301   | TGACAGTGTGTTTGGCCCTCAAGTTTGTCTAGCTGCTGGTTTATTAAGTAAAGAAAGATGT 360   |
| Db                         | 301   | TGACAGTGTGTTTGGCCCTCAAGTTTGTCTAGCTGCTGGTTTATTAAGTAAAGAAAGATGT 360   |
| Qy                         | 361   | GGCAGATTGTTTCTTTTACTCTCAGCTGTGATCTTGTGTCGCGCAGCTATAAACAAT 420       |
| Db                         | 361   | GGCAGATTGTTTCTTTTACTCTCAGCTGTGATCTTGTGTCGCGCAGCTATAAACAAT 420       |
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| Db                         | 421   | TTCCGAAGAGCATGGACAGCATAGGAAAGAAAGCAATATCAGGTCCAGCATGGGTCCCTGCA 480  |
| Qy                         | 481   | GCTACACTTTCTCTCCAGAGATGACAACTGCGCTCTTCTCCAGCCCTTACCTGT 540          |
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| Db                         | 601   | TGCTGGAGAACATCATGTGAAAAACAACTCAGTGGCTTAATGAAGCTTGAGAAATATATATCC 660 |
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| Db                         | 661   | AGGACCAATGAAGAAAGAAATGCTAGAGATACAGCAGAAATGCAATCAGAACCCAGACGG 720    |
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| Db                         | 721   | CTGTGATGATAGAAATAGGGACAAAACCTGTTGAAACCAACAGCTGAGCAAAACCGGGAAGT 780  |
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| Db                         | 781   | TAACTGATGGAAGCCAAAGTATTAATCAGACCCAGACTTTGAACTTCAGCTCTTGG 840        |
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Db 1141 TGTCACATCAAACTCAGCTAAGAGCCCACTGTTGCTTAAAGAGAAACAAATCAGCTTCA 1200
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RESULT 5
LOCUS AR403899 2282 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6627415.
ACCESSION AR403899
VERSION AR403899.1 GI:40151796
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2282)
AUTHORS Davis,S. and Yancopoulos,G.D.
TITLE TIE-2 ligands, methods of making and uses thereof
JOURNAL Patent: US 6627415-A 5 30-SEP-2003;
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## RESULT 6

AR429415

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

2282 bp DNA linear PAT 18-DEC-2003  
Sequence 5 from patent US 6645484.

AR429415

AR429415

AR429415.1

GI:40189610

Unknown.

Unclassified.

1 (bases 1 to 2282)

Davis, S., Bruno, J., Goldfarb, M., Aldrich, T. H., Maisonnier, P. C.,  
Radziejewski, C., Jones, P. F. and Yancopoulos, G. D.

|  |                     |  |     |  |  |  |  |  |  |
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| TITLE<br>Method of blocking blood vessel growth using tie-2 ligand 2 |                     |  |     |  |  |  |  |  |  |
| JOURNAL<br>Patent: US 6645484-A 5 11-NOV-2003;                       |                     |  |     |  |  |  |  |  |  |
| FEATURES<br>Location/Qualifiers                                      |                     |  |     |  |  |  |  |  |  |
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| Query Match 100.0%; Score 2282; DB 6; Length 2282;                   |                     |  |     |  |  |  |  |  |  |
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| Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;        |                     |  |     |  |  |  |  |  |  |
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| Db   | 1                   | GAATTCCTGGTGGTGTATTACTCTCTCCAGCCTTGAGGGAGGAACAACACTGTAGGA      | 60  |  |  |  |  |  |  |
| QY   | 61                  | TCGTGGGAGAGAGGAACAAGACCGTGAAAGCTGCTCTGTAAAGCTGTACACAGCCCTC     | 120 |  |  |  |  |  |  |
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| Db   | 121                 | CCAAGTGACGAGCACTGTTCTTCCCACTGCAATCTGACAGTTTACTTGCATGCTCGAGAG   | 180 |  |  |  |  |  |  |
| QY   | 181                 | AACACAGCAGTAAAAACAGAGTTTGCTACTCGAAAAAGGAAGAAGAGACTTTCATTG      | 240 |  |  |  |  |  |  |
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| QY   | 241                 | ACGGACCCAGCCATGGCAGCGTAGCGCCCTGCTTTTACAGCGCAGCAGCTCGGAGCTC     | 300 |  |  |  |  |  |  |
| Db   | 241                 | ACGGACCCAGCCATGGCAGCGTAGCGCCCTGCGCTTTACAGCGCAGCAGCTCGGAGCTC    | 300 |  |  |  |  |  |  |
| QY   | 301                 | TGGACGTGTGTTGGCCCTCAAGTTTGTCTAAAGCTGCTGCTTATTACTGAAGAAAGAATGT  | 360 |  |  |  |  |  |  |
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| Db   | 421                 | TTCCGAAGAGCATGACAGCATAGGAAGAGCAATATCAGTCCAGCATGGGTCTGCA        | 480 |  |  |  |  |  |  |
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| QY   | 541                 | CCAAATGCTGTGCAGAGGACGCGCGCTCGAATACGATGACTCGGTGCGAGAGGCTCAAG    | 600 |  |  |  |  |  |  |
| Db   | 541                 | CCAAATGCTGTGCAGAGGACGCGCGCTCGAATACGATGACTCGGTGCGAGAGGCTCAAG    | 600 |  |  |  |  |  |  |
| QY   | 601                 | TGCTGGAGAACATCATGGAACAACAACACTCAGTGGCTAATGAAGCTTGAGAAATTATCC   | 660 |  |  |  |  |  |  |
| Db   | 601                 | TGCTGGAGAACATCATGGAACAACAACACTCAGTGGCTAATGAAGCTTGAGAAATTATCC   | 660 |  |  |  |  |  |  |
| QY   | 661                 | AGGACAAACATGAAGAAAGAAATGGTAGAGATACAGCAGAAATGCAAGTACAGAACCGACGG | 720 |  |  |  |  |  |  |
| Db   | 661                 | AGGACAAACATGAAGAAAGAAATGGTAGAGATACAGCAGAAATGCAAGTACAGAACCGACGG | 720 |  |  |  |  |  |  |
| QY   | 721                 | CTGTGATGATAGAAATAGGGACAAACCTGTTGAAACCAACAGCTGAGCAAAACGCGAAGT   | 780 |  |  |  |  |  |  |
| Db   | 721                 | CTGTGATGATAGAAATAGGGACAAACCTGTTGAAACCAACAGCTGAGCAAAACGCGAAGT   | 780 |  |  |  |  |  |  |
| QY   | 781                 | TAACTGATGTGAAGCCCAAGTATTAAATCAGACCAAGACTTGAACCTTACGCTCTTGG     | 840 |  |  |  |  |  |  |
| Db   | 781                 | TAACTGATGTGAAGCCCAAGTATTAAATCAGACCAAGACTTGAACCTTACGCTCTTGG     | 840 |  |  |  |  |  |  |
| QY   | 841                 | AACACTCCCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCAAGCCAGTGAATAA   | 900 |  |  |  |  |  |  |
| Db   | 841                 | AACACTCCCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCAAGCCAGTGAATAA   | 900 |  |  |  |  |  |  |
| QY   | 901                 | ACAAATTGCAAGATTAAGAACAGTTCCTCTAGAAAAAGAGGTCTAGCTTATGGAAGACAAGC | 960 |  |  |  |  |  |  |

|    |      |  |      |  |  |  |  |  |  |
|----|------|--|------|--|--|--|--|--|--|
| DB | 901  | ACAAATTGCAAGATAAGAACAGTCTTCTAGAAAAAGAGGTGTAGCTATGGAAGACAAGC  | 960  |  |  |  |  |  |  |
| QY | 961  | ACATCATCCAACTCAGTCAATATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCA  | 1020 |  |  |  |  |  |  |
| DB | 961  | ACATCATCCAACTCAGTCAATATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCA  | 1020 |  |  |  |  |  |  |
| QY | 1021 | AGCAAAATTTCCATCAATGAAGAACTAGAAAAAATAATAGTCACTGCCCGGTGAATAATT | 1080 |  |  |  |  |  |  |
| DB | 1021 | AGCAAAATTTCCATCAATGAAGAACTAGAAAAAATAATAGTCACTGCCCGGTGAATAATT | 1080 |  |  |  |  |  |  |
| QY | 1081 | CAGTTCTTCAAAGCAGCAACATGATCTCATGGAGACAGTTAAATACTTACTGACTATGA  | 1140 |  |  |  |  |  |  |
| DB | 1081 | CAGTTCTTCAAAGCAGCAACATGATCTCATGGAGACAGTTAAATACTTACTGACTATGA  | 1140 |  |  |  |  |  |  |
| QY | 1141 | TGTCACACATCAAACTCAGTAAAGACCCCACTGTTGCTAAAGAAACAAATCAGCTTCA   | 1200 |  |  |  |  |  |  |
| DB | 1141 | TGTCACACATCAAACTCAGTAAAGACCCCACTGTTGCTAAAGAAACAAATCAGCTTCA   | 1200 |  |  |  |  |  |  |
| QY | 1201 | GAGACTGTGCTGAAGTATTTCAAATCAGGACACACACAAATGGCATCTACAGTTAAACAT | 1260 |  |  |  |  |  |  |
| DB | 1201 | GAGACTGTGCTGAAGTATTTCAAATCAGGACACACACAAATGGCATCTACAGTTAAACAT | 1260 |  |  |  |  |  |  |
| QY | 1261 | TCCCTAAATTTACAGAAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGAGCGGT   | 1320 |  |  |  |  |  |  |
| DB | 1261 | TCCCTAAATTTACAGAAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGAGCGGT   | 1320 |  |  |  |  |  |  |
| QY | 1321 | GGACAATTTTTCAGCGAGCTGAGGATGCGGTTGATTTTCAGAGGACTTTGGAAGAAT    | 1380 |  |  |  |  |  |  |
| DB | 1321 | GGACAATTTTTCAGCGAGCTGAGGATGCGGTTGATTTTCAGAGGACTTTGGAAGAAT    | 1380 |  |  |  |  |  |  |
| QY | 1381 | ATAAGTGGGATTTGGTAAACCTTTCAGGAGAAATATGCTGGGAAATGAGTTTTCGCG    | 1440 |  |  |  |  |  |  |
| DB | 1381 | ATAAGTGGGATTTGGTAAACCTTTCAGGAGAAATATGCTGGGAAATGAGTTTTCGCG    | 1440 |  |  |  |  |  |  |
| QY | 1441 | AACAGCTAAATCAGCAACCGCTATGCTTAAATAACACCTTAAAGACTGGGAGGGAATG   | 1500 |  |  |  |  |  |  |
| DB | 1441 | AACAGCTAAATCAGCAACCGCTATGCTTAAATAACACCTTAAAGACTGGGAGGGAATG   | 1500 |  |  |  |  |  |  |
| QY | 1501 | AGGCTTACTCATTTGATGAACAATTTCTCTCAAGTGAAGAACTCAATATATAGATTTC   | 1560 |  |  |  |  |  |  |
| DB | 1501 | AGGCTTACTCATTTGATGAACAATTTCTCTCAAGTGAAGAACTCAATATATAGATTTC   | 1560 |  |  |  |  |  |  |
| QY | 1561 | ACCTTAAAGAGCTTACAGGGAAGCCGCAAAATAAGCAGCATCAGCCAAACAGGAAATG   | 1620 |  |  |  |  |  |  |
| DB | 1561 | ACCTTAAAGAGCTTACAGGGAAGCCGCAAAATAAGCAGCATCAGCCAAACAGGAAATG   | 1620 |  |  |  |  |  |  |
| QY | 1621 | ATTTTAGCAACAAGATGGAGACAAGACAATGTTTTCGAAATGTTTCAAAATGCTTAA    | 1680 |  |  |  |  |  |  |
| DB | 1621 | ATTTTAGCAACAAGATGGAGACAAGACAATGTTTTCGAAATGTTTCAAAATGCTTAA    | 1680 |  |  |  |  |  |  |
| QY | 1681 | CAGGAGGCTGGTGGTTCGATGCTGCTTCCAACTTGAACGGAATGTACTATCCAC       | 1740 |  |  |  |  |  |  |
| DB | 1681 | CAGGAGGCTGGTGGTTCGATGCTGCTTCCAACTTGAACGGAATGTACTATCCAC       | 1740 |  |  |  |  |  |  |
| QY | 1741 | AGAGGACAAACAAATAAGTTCAACGGCATTTAAATGTTACTCTGGAAGGCTCAGGCT    | 1800 |  |  |  |  |  |  |
| DB | 1741 | AGAGGACAAACAAATAAGTTCAACGGCATTTAAATGTTACTCTGGAAGGCTCAGGCT    | 1800 |  |  |  |  |  |  |
| QY | 1801 | ATTGCTCAAGGCCAACAACCATGATGATCCGACAGCAGATTTCTAAACATCCAGTCCA   | 1860 |  |  |  |  |  |  |
| DB | 1801 | ATTGCTCAAGGCCAACAACCATGATGATCCGACAGCAGATTTCTAAACATCCAGTCCA   | 1860 |  |  |  |  |  |  |
| QY | 1861 | CCTGAGGAACCTGCTCGAACTATTTTCAAGACTTAAAGCAGTGCATGAAAGTCAAGG    | 1920 |  |  |  |  |  |  |
| DB | 1861 | CCTGAGGAACCTGCTCGAACTATTTTCAAGACTTAAAGCAGTGCATGAAAGTCAAGG    | 1920 |  |  |  |  |  |  |
| QY | 1921 | CTGGCACTGTGCTCTTCCACCAAGAGGCGGTGCTCGGTGCTGACGCGACCCACA       | 1980 |  |  |  |  |  |  |
| DB | 1921 | CTGGCACTGTGCTCTTCCACCAAGAGGCGGTGCTCGGTGCTGACGCGACCCACA       | 1980 |  |  |  |  |  |  |
| QY | 1981 | TGCTCAGATTAGAGCCTGTGTAACCTTTTATCATTTAACTTGCATCATTAACGGAACCAA | 2040 |  |  |  |  |  |  |
| DB | 1981 | TGCTCAGATTAGAGCCTGTGTAACCTTTTATCATTTAACTTGCATCATTAACGGAACCAA | 2040 |  |  |  |  |  |  |

Db 1981 TGCTCAGATTAGAGCTGTAACTTTATCACTTAACTTGCATCACTTAAACGGACCAA 2040  
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Db 2041 GCAAGACCTTAAACATCCATAATTTGATTTAGACAGAACACCTTATGCAAGATGAACCG 2100  
QY 2101 AGCTCAGAAATCAGACTGACAGTTTACAGACGCTGTCTGACAAACCAAGAAATGTTATGTG 2160  
Db 2101 AGCTCAGAAATCAGACTGACAGTTTACAGACGCTGTCTGACAAACCAAGAAATGTTATGTG 2160  
QY 2161 CRAAGTTTATCAGTAATAAATCTGGAAACAGAACACATTTATGTTATACAATACAGATCATCT 2220  
Db 2161 CAAGTTTATCAGTAATAAATCTGGAAACAGAACACATTTATGTTATACAATACAGATCATCT 2220  
QY 2221 TGGAACTGCAATCTTCTGAGCACTGTTTATACACTGTGTAAATPACCATATGTCCTGAAT 2280  
Db 2221 TGGAACTGCAATCTTCTGAGCACTGTTTATACACTGTGTAAATPACCATATGTCCTGAAT 2280  
QY 2281 TC 2282  
Db 2281 TC 2282

RESULT 7  
ARI76322  
LOCUS  
DEFINITION Sequence 3 from patent US 6312694.  
ACCESSION ARI76322  
VERSION ARI76322.1 GI:17918677  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2269)  
AUTHORS Thorpe, P.E. and Ran, S.  
TITLE Cancer treatment methods using therapeutic conjugates that bind to  
JOURNAL aminophospholipids  
Patent: US 6312694-A 3 06-NOV-2001;  
FEATURES Location/Qualifiers  
source 1..2269  
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ORIGIN  
Query Match 99.4%; Score 2269; DB 6; Length 2269;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGGTTGGTGTGTTATCTCTCCAGCCTTGAGGAGGGAACAACACTGTAGGATCTGGGG 67  
Db 1 TGGGTTGGTGTGTTATCTCTCCAGCCTTGAGGAGGGAACAACACTGTAGGATCTGGGG 60  
QY 68 AGAGAGAAACAAGGACCGTGAAGCTGCTGTGTAAAGCTGACACAGCCCTCCCAAGTG 127  
Db 61 AGAGAGAAACAAGGACCGTGAAGCTGCTGTGTAAAGCTGACACAGCCCTCCCAAGTG 120  
QY 128 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGATGCTGGAGAGAACACAG 187  
Db 121 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGATGCTGGAGAGAACACAG 180  
QY 188 CAGTAAAAACACAGGTTTGTCTACTGGAAAAAGAGAAAGAGAAAGTTCATTGACGGACC 247  
Db 181 CAGTAAAAACAGGTTTGTCTACTGGAAAAAGAGAAAGAGAAAGTTCATTGACGGACC 240  
QY 248 CAGCCATGGCAGCTAGACGCCCTCGGTTTCAGACGGCAGCAGCTCGGACTCTGGACGT 307  
Db 241 CAGCCATGGCAGCTAGACGCCCTCGGTTTCAGACGGCAGCAGCTCGGACTCTGGACGT 300  
QY 308 GTGTTTGGCCTCAAGTTTGTCTAAGCTGCTGTTTATTACTGAAGAAAGAAATGTGCGCAGAT 367  
Db 301 GTGTTTGGCCTCAAGTTTGTCTAAGCTGCTGTTTATTACTGAAGAAAGAAATGTGCGCAGAT 360  
QY 368 TGTTTCTTTTACTCTGAGCTGTGATCTGTCTTGGCCGCGAGCCCTATAACAACTTTCGGAA 427

Db 361 TGTTCCTTTTACTCTGAGCTGTGATCTTCTTGGCCGCGAGCTTAAACAACCTTTCGGAA 420  
QY 428 GAGCATGGGACAGCATAGGAAAGAACATATCAGGTCAGCATGGGTCTCTGAGCTACAC 487  
Db 421 GAGCATGGGACAGCATAGGAAAGAACATATCAGGTCAGCATGGGTCTCTGAGCTACAC 480  
QY 488 TTTCTCTCTCCAGAGATGGACAACTGCGCTCTTCTCCAGCCCTCAGTGTCCAATGC 547  
Db 481 TTTCTCTCTCCAGAGATGGACAACTGCGCTCTTCTCCAGCCCTCAGTGTCCAATGC 540  
QY 548 TGTGACAGGGGACGCGCCGCTCGAATACGATGACTCGGTGACAGGCTGCAAGTGTGGA 607  
Db 541 TGTGACAGGGGACGCGCCGCTCGAATACGATGACTCGGTGACAGGCTGCAAGTGTGGA 600  
QY 608 GAAACATCATGGAAAAACAACAACACTCAGTGGCTTAATGAAGCTTGAGAAATATATCCAGACAA 667  
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QY 668 CATGAAGAAAGAAATGCTAGAGATACAGCAGATGCAAGTACAGAACCCAGCGCTGTGAT 727  
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QY 728 GATAGAAATAGGACAAACCTGTTGAACCAACAGCTGAGCAAAACCGGGAAGTTAACTGA 787  
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QY 968 CCAACTACAGTCAATTAAGAGAGAGAAAGATCAGCTACAGGTGTATGATATCCAAGCAAAA 1027  
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Db 1081 TCAAAAGCAGACATGATCTCATGGACAGTTTAATACTTACTGACTATGATGTCAC 1140  
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Db 1141 ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAGAGAAACAATCAGCTTCAGAGACTG 1200  
QY 1208 TGCTGAAGTATTCAAAATCAGGACACACCAAAATGGCATCTACAGTTTAACATTTCCCTAA 1267  
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QY 1328 TATTTCAGCGAGCTGAGGATGGCAGCGTTGATTTTTCAGAGGACTTGGAAAGAAATAAAGT 1387  
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QY 1388 GGGATTTGGTAAACCTTTACAGAGAAATATGGCTGGGAAATGAGTTTGTTCGCAACTGAC 1447  
Db 1381 GGGATTTGGTAAACCTTTACAGAGAAATATGGCTGGGAAATGAGTTTGTTCGCAACTGAC 1440  
QY 1448 TAATCAGCAACGCTATGTGCTTAAATACACCTTAAAGACTGGGAAGGATGAGGCTTA 1507









| Best Local Similarity 100.0%; Pred. No. 0;                    |      |   |      |
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| Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |      |   |      |
| Qy  | 8    | TGGGTTGGTGTATCTCTCCAGCCTTGAGGAGGGAACAAACATCTGTAGGATCTGGG      | 67   |
| Db  | 1    | TGGGTTGGTGTATCTCTCCAGCCTTGAGGAGGGAACAAACATCTGTAGGATCTGGG      | 60   |
| Qy  | 68   | AGAGAGAAACAAAGGACCGTGAAGCTGCTCTGTATAAGCTGACACAGCCCTCCCAAGTG   | 127  |
| Db  | 61   | AGAGAGAAACAAAGGACCGTGAAGCTGCTCTGTATAAGCTGACACAGCCCTCCCAAGTG   | 120  |
| Qy  | 128  | AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGCTGGAGAGACACAG     | 187  |
| Db  | 121  | AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGCTGGAGAGACACAG     | 180  |
| Qy  | 188  | CAGTAAAAACCCAGGTTTGTCTACTGCAAAAAAGAGAGAAAGACTTTTCATTGACGAC    | 247  |
| Db  | 181  | CAGTAAAAACCCAGGTTTGTCTACTGCAAAAAAGAGAGAAAGACTTTTCATTGACGAC    | 240  |
| Qy  | 248  | CAGCCATGGCAGCTAGCAGCCCTGCGTTTCAGACGCGCAGCTCGGAGCTCTGGA        | 307  |
| Db  | 241  | CAGCCATGGCAGCTAGCAGCCCTGCGTTTCAGACGCGCAGCTCGGAGCTCTGGA        | 300  |
| Qy  | 308  | GTGTTTGGCCTCAAGTTTGTCTAAGCTGCTGTTTATTACTGAAGAAAGATGTGGAGAT    | 367  |
| Db  | 301  | GTGTTTGGCCTCAAGTTTGTCTAAGCTGCTGTTTATTACTGAAGAAAGATGTGGAGAT    | 360  |
| Qy  | 368  | TGTTTTCTTTACTCTGAGCTGTGATCTTGTTCTGGCGCGCAGCCTATAAACACTTTTCG   | 427  |
| Db  | 361  | TGTTTTCTTTACTCTGAGCTGTGATCTTGTTCTGGCGCGCAGCCTATAAACACTTTTCG   | 420  |
| Qy  | 428  | GAGCATGGACAGCATAGGAAAGAGCAATATCAGGTCAGCATGGGTCCTGCAAGCTACAC   | 487  |
| Db  | 421  | GAGCATGGACAGCATAGGAAAGAGCAATATCAGGTCAGCATGGGTCCTGCAAGCTACAC   | 480  |
| Qy  | 488  | TTTCTCTCTGCGAGATGGAACACTGCGGCTCTTCTCCAGCCCTTACGTTGCCAATGC     | 547  |
| Db  | 481  | TTTCTCTCTGCGAGATGGAACACTGCGGCTCTTCTCCAGCCCTTACGTTGCCAATGC     | 540  |
| Qy  | 548  | TGTCAGAGGACGCGCGCTCGAATACGATGACTCGGTGCGAGGCTGCAAGTCTGGA       | 607  |
| Db  | 541  | TGTCAGAGGACGCGCGCTCGAATACGATGACTCGGTGCGAGGCTGCAAGTCTGGA       | 600  |
| Qy  | 608  | GAAATCATGGAACAAACACTCAGTGGCTTAATGAAGCTTGAGAAATATATCCAGGACAA   | 667  |
| Db  | 601  | GAAATCATGGAACAAACACTCAGTGGCTTAATGAAGCTTGAGAAATATATCCAGGACAA   | 660  |
| Qy  | 668  | CATGAAGAAAGATGTTAGATACAGCAGAAATGCAAGTTCAGAAACAGACGCTGTGAT     | 727  |
| Db  | 661  | CATGAAGAAAGATGTTAGATACAGCAGAAATGCAAGTTCAGAAACAGACGCTGTGAT     | 720  |
| Qy  | 728  | GATGAAGATAGGACAAACCTGTTGAACCAACAGCTGAGCAACGCGGAGTTTAACTGA     | 787  |
| Db  | 721  | GATGAAGATAGGACAAACCTGTTGAACCAACAGCTGAGCAACGCGGAGTTTAACTGA     | 780  |
| Qy  | 788  | TGTGGAAGCCCAAGTATTAAATCAGACAGACACTTGAACCTTCAGCTCTTGGAAACACTC  | 847  |
| Db  | 781  | TGTGGAAGCCCAAGTATTAAATCAGACCAAGACTTGAACCTTCAGCTCTTGGNACACTC   | 840  |
| Qy  | 848  | CCTCTCGACAAACAAATTTGGAACAAACAGATTTTGGACCGACCAAGTGAATAAACAAATT | 907  |
| Db  | 841  | CCTCTCGACAAACAAATTTGGAACAAACAGATTTTGGACCGACCAAGTGAATAAACAAATT | 900  |
| Qy  | 908  | GCAAGATAGAACAGTTTCTAGAAAAGAGTGCTAGCTATGGAAGACAGACATCAT        | 967  |
| Db  | 901  | GCAAGATAGAACAGTTTCTAGAAAAGAGTGCTAGCTATGGAAGACAGACATCAT        | 960  |
| Qy  | 968  | CCAACTACAGTCAATATAAGAGAGAAAGATCAGCTACAGGTGTAGCTATCCAGGACAAA   | 1027 |
| Db  | 961  | CCAACTACAGTCAATATAAGAGAGAAAGATCAGCTACAGGTGTAGCTATCCAGGACAAA   | 1020 |
| Qy  | 1028 | TTCCATCATTTGAAGAACTAGAAAAAAAATAGTCACTGCCACGGTGAATAATTCAAGTTCT | 1087 |

QY 2168 ATCAGTAAATAACTGGAAACAGAACACTTATGTTATACAAATACAGATCATCTTGGAACT 2227  
DB 2161 ATCAGTAAATAACTGGAAACAGAACACTTATGTTATACAAATACAGATCATCTTGGAACT 2220  
QY 2228 GCATTTCTTGTAGCACTGTTTATACACTGTGTAAATACCCATATGTCCT 2276  
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ARI83468  
LOCUS ARI83468 2269 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 3 from patent US 6342219.  
ACCESSION ARI83468  
VERSION ARI83468.1 GI:20227437  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2269)  
AUTHORS Thorpe, P.E. and Brekken, R.A.  
TITLE Antibody compositions for selectively inhibiting VEGF  
JOURNAL Patent: US 6342219-A 3 29-JAN-2002;  
FEATURES  
Location/Qualifiers  
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ORIGIN  
Query Match 99.4%; Score 2269; DB 6; Length 2269;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 TGGGTGGTGTATCTCTCCAGCCTTGAGGAGGGAACACACTGTAGGATCTGGGG 67  
DB 1 TGGGTGGTGTATCTCTCCAGCCTTGAGGAGGGAACACACTGTAGGATCTGGGG 60  
QY 68 AGAGAGGAACAAGAGCCGTGMAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG 127  
DB 61 AGAGAGGAACAAGAGCCGTGMAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG 120  
QY 128 AGCAGGACTGTCTTCCCACTGCAATCTGCAGCTTTACTGCATGCTCTGGAGAGAACACAG 187  
DB 121 AGCAGGACTGTCTTCCCACTGCAATCTGCAGCTTTACTGCATGCTCTGGAGAGAACACAG 180  
QY 188 CAGTAAACACAGGTTTGCTACTGGAACAGAGAGAGAGAGACTTTTCAATGACGAC 247  
DB 181 CAGTAAACACAGGTTTGCTACTGGAACAGAGAGAGAGAGACTTTTCAATGACGAC 240  
QY 248 CAGCATGGCAGCTAGCAGCCCTGCTTTCAGACGCGCAGCAGCTCGGGACTCTGGACGT 307  
DB 241 CAGCATGGCAGCTAGCAGCCCTGCTTTCAGACGCGCAGCAGCTCGGGACTCTGGACGT 300  
QY 308 GTGTTTCCCTCAAGTTTGCTAAGCTGCTGTTTATTACTGAAGAAAGAAATGTGGCAGAT 367  
DB 301 GTGTTTCCCTCAAGTTTGCTAAGCTGCTGTTTATTACTGAAGAAAGAAATGTGGCAGAT 360  
QY 368 TGTGTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCGCGAGCCTATACAACTTTCGAA 427  
DB 361 TGTGTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCGCGAGCCTATACAACTTTCGAA 420  
QY 428 GAGCATGCACGATAGGAAGAGCAATATCAGTCCAGCATGGTCTGACGTACAC 487  
DB 421 GAGCATGCACGATAGGAAGAGCAATATCAGTCCAGCATGGTCTGACGTACAC 480  
QY 488 TTTCTCTCTGCGCAGAGATGGAACAACCTGCTTCTTCCAGCCCTTACGTGTCATGTC 547  
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QY 548 TGTGAGAGGACCGCGCTGCAATACGATGATCTCGGTGAGAGGCTGCAAGTGTGGA 607  
DB 541 TGTGAGAGGACCGCGCTGCAATACGATGATCTCGGTGAGAGGCTGCAAGTGTGGA 600

QY 608 GAACATCATGGAAACAACTCAGTGGCTTAATGAAGCTTGAAATATATATCCAGGACAA 667  
DB 601 GAACATCATGGAAACAACTCAGTGGCTTAATGAAGCTTGAAATATATATCCAGGACAA 660  
QY 668 CATGAAGAAGAAATGCTAGAGATACAGCAGAAATGAGTACAGAACCCAGCGCTGTGAT 727  
DB 661 CATGAAGAAGAAATGCTAGAGATACAGCAGAAATGAGTACAGAACCCAGCGCTGTGAT 720  
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DB 721 GATAGAAATAGGACAAACCTGTTGAACCAACAGCTGAGCAACCGCGGAAGTTAACTGA 780  
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DB 1081 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTAACTTACTGATATGATGTCCAC 1140  
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DB 1141 ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAGAACAAATCAGCTTCAGAGACTG 1200  
QY 1208 TGCTGAGTATTCAAATCAGGACACACCAAAATGGCATCTACACGTTTAACTTCCCTAA 1267  
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DB 1261 TTCTACAGAGAGATCAAGGCTTACTGTGACATGGAACTGGAGAGCGGGTGGACAAT 1320  
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DB 1321 TATTCAGCGACGTGAGGATGGCAGCGTTGATTTTTCAGAGGACTTTGGAAGAAATATAAGT 1380  
QY 1388 GGGATTTGGTAAACCTTCAGGAGAAATATGGCTGGGAATAGTTCGCGAACTGAC 1447  
DB 1381 GGGATTTGGTAAACCTTCAGGAGAAATATGGCTGGGAATAGTTCGCGAACTGAC 1440  
QY 1448 TAATCAGCAACGCTATGCTTAAATAACACCTTTAAAGACTGGGAAGGAAATGAGGCTTA 1507  
DB 1441 TAATCAGCAACGCTATGCTTAAATAACACCTTTAAAGACTGGGAAGGAAATGAGGCTTA 1500  
QY 1508 CTCAATTGATGAACATTTCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1567  
DB 1501 CTCAATTGATGAACATTTCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1560  
QY 1568 AGGATTTACAGGACAGCCCGCAAAATAAGCAGCATCAGCCCAACCCAGGAATGATTTAG 1627  
DB 1561 AGGATTTACAGGACAGCCCGCAAAATAAGCAGCATCAGCCCAACCCAGGAATGATTTAG 1620  
QY 1628 CACAAAGGATGGAGACAAACGACAAATCTATTGCAAAATGTTTCAAAATGCTTAAACAGGAGG 1687  
DB 1621 CACAAAGGATGGAGACAAACGACAAATGTTTTCGAAATGTTTCAAAATGCTTAAACAGGAGG 1680

|                            |      |   |      |
|----------------------------|------|---|------|
| Qy                         | 1588 | CTGTGTTGATGCATGTGGTCTTCCAACTTGAACGGAAATGATCTATCAACAGAGCCA       | 1747 |
| Db                         | 1681 | CTGTGTTGTTGATGCATGTGGTCTTCCAACTTGAACGGAAATGATCTATCAACAGAGCCA    | 1740 |
| Qy                         | 1748 | GAACACAAATAAGTTCAACGGCATTAATGGTACTACTGGAAGGCTCAGGCTATTGGCT      | 1807 |
| Db                         | 1741 | GAACACAAATAAGTTCAACGGCATTAATGGTACTACTGGAAGGCTCAGGCTATTGGCT      | 1800 |
| Qy                         | 1808 | CAAGGCCACAACCATGATGATCCGACACAGACAGATTCTTAAACATCCCGAGTCCACCTGAGG | 1867 |
| Db                         | 1801 | CNAGGCCACAACCATGATGATCCGACACAGACAGATTCTTAAACATCCCGAGTCCACCTGAGG | 1860 |
| Qy                         | 1868 | AACGTGCTCGAACTATTTTCAAAGACTTAAAGCCAGTGCACCTGAAGAGTCAAGGCTGCGCA  | 1927 |
| Db                         | 1861 | AACGTGCTCGAACTATTTTCAAAGACTTAAAGCCAGTGCACCTGAAGAGTCAAGGCTGCGCA  | 1920 |
| Qy                         | 1928 | CTGTGTTCTCTTCCACACAGAGGGCGTGTGCTGCTGCTGACGGGACCCACATGCTCCA      | 1987 |
| Db                         | 1921 | CTGTGTTCTCTTCCACACAGAGGGCGTGTGCTGCTGCTGACGGGACCCACATGCTCCA      | 1980 |
| Qy                         | 1988 | GATTAGAGCCCTGTAAACTTTTATCACTTAACTTGCATCACTTAAACGGACCAAGCAAGAC   | 2047 |
| Db                         | 1981 | GATTAGAGCCCTGTAAACTTTTATCACTTAACTTGCATCACTTAAACGGACCAAGCAAGAC   | 2040 |
| Qy                         | 2048 | CCTAAACATCATTAATTTGATTAAGACAGAACACCTATGCAAAAGATGAACCCGAGGCTGA   | 2107 |
| Db                         | 2041 | CCTAAACATCATTAATTTGATTAAGACAGAACACCTATGCAAAAGATGAACCCGAGGCTGA   | 2100 |
| Qy                         | 2108 | GAATCAGACTGACAGTTTACAGAGCTGCTGTCAACACCAAGATGTTATGTGCAAGTTT      | 2167 |
| Db                         | 2101 | GAATCAGACTGACAGTTTACAGAGCTGCTGTCAACACCAAGATGTTATGTGCAAGTTT      | 2160 |
| Qy                         | 2168 | ATCAGTAAATAACTTGGAAAAACAGAACTTATGTTATACAAATACAGATCATCTTGGAACT   | 2227 |
| Db                         | 2161 | ATCAGTAAATAACTTGGAAAAACAGAACTTATGTTATACAAATACAGATCATCTTGGAACT   | 2220 |
| Qy                         | 2228 | GCATTTCTTGACACTGTTTATACACTGTGTAAATACCCATATGTCT                  | 2276 |
| Db                         | 2221 | GCATTTCTTGACACTGTTTATACACTGTGTAAATACCCATATGTCT                  | 2269 |
| RESULT 11                  |      |   |      |
| AR183517                   |      |   |      |
| LOCUS                      |      |   |      |
| DEFINITION                 |      |   |      |
| ACCESSION                  |      |   |      |
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| Qy                         | 8    | TGGGTTGGTGTATTATCTCTCCAGCCCTTGAGGGAGGAAACAACATGTAGGATCTGGGG     | 67   |
| Db                         | 1    | TGGGTTGGTGTATTATCTCTCCAGCCCTTGAGGGAGGAAACAACATGTAGGATCTGGGG     | 60   |
| Qy                         | 68   | AGAGAGAAACAAAGGACCGTGAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG      | 127  |
| Db                         | 61   | AGAGAGAAACAAAGGACCGTGAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG      | 120  |

|  |    |      |  |      |
|--|----|------|--|------|
|  | Db | 1201 | TGCTGAAGTATTCAAATCAGGCACACCACAATGGCACTTACCGTTAACTTCCTCTAA        | 1260 |
|  | Qy | 1268 | TTCTACAGAAGAGATCAAGCCCTACTGTGACATCGAAGCTGGAGGAGCGGGTSGACAAT      | 1327 |
|  | Db | 1261 | TTCTACAGAAGAGATCAAGCCCTACTGTGACATCGAAGCTGGAGGAGCGGGTGGACAAT      | 1320 |
|  | Qy | 1328 | TATTCAGCGCATGTGAGGATGGCAGCGTTGATTTTTCAGAGACCTTGGAAGAAATATAAAGT   | 1387 |
|  | Db | 1321 | TATTCAGCGCATGTGAGGATGGCAGCGTTGATTTTTCAGAGACCTTGGAAGAAATATAAAGT   | 1380 |
|  | Qy | 1388 | GGGATTTGGTAAACCCCTTCAGGAGAAATTCGCTGGGAAAATGAGTTTGTTCGCAACTGAC    | 1447 |
|  | Db | 1381 | GGGATTTGGTAAACCCCTTCAGGAGAAATTCGCTGGGAAAATGAGTTTGTTCGCAACTGAC    | 1440 |
|  | Qy | 1448 | TAAATCAGCAACGCTATGTGCTTAAAAATACACCTTAAAGACTGGGAAGGGAATCAGGCTTA   | 1507 |
|  | Db | 1441 | TAAATCAGCAACGCTATGTGCTTAAAAATACACCTTAAAGACTGGGAAGGGAATCAGGCTTA   | 1500 |
|  | Qy | 1508 | CTCATTTGATGAACATTTCTTATCTCTCAAGTAGAAGAACTCAATATATAGGATTCACCTTAA  | 1567 |
|  | Db | 1501 | CTCATTTGATGAACATTTCTTATCTCTCAAGTAGAAGAACTCAATATATAGGATTCACCTTAA  | 1560 |
|  | Qy | 1568 | AGGACTTTACAGGGACAGCCGCCAAAATAAGCAGCATCAGCCAACCCAGGAAGATCATTTTAG  | 1627 |
|  | Db | 1561 | AGGACTTTACAGGGACAGCCGCCAAAATAAGCAGCATCAGCCAACCCAGGAAGATCATTTTAG  | 1620 |
|  | Qy | 1628 | CACAAAGGATGGAGAACACGACAAATGTATTTGCCAAATGTTTCAAAATGCTTAACAGGAGG   | 1687 |
|  | Db | 1621 | CACAAAGGATGGAGAACACGACAAATGTATTTGCCAAATGTTTCAAAATGCTTAACAGGAGG   | 1680 |
|  | Qy | 1688 | CTGGTGTGTTGATGCATGTGGTCTCTTCCAACTTGAAACGGAAATGTATCTATCCACAGAGGCA | 1747 |
|  | Db | 1681 | CTGGTGTGTTGATGCATGTGGTCTCTTCCAACTTGAAACGGAAATGTATCTATCCACAGAGGCA | 1740 |
|  | Qy | 1748 | GAAACAAATTAAGTTTCAACGGCATTAATGTGTACTACTGGAAGGCTCAGGCTATTGCGT     | 1807 |
|  | Db | 1741 | GAAACAAATTAAGTTTCAACGGCATTAATGTGTACTACTGGAAGGCTCAGGCTATTGCGT     | 1800 |
|  | Qy | 1808 | CAAGGCCACAACCATGATGATGCCACAGCAGAGATTTCTTAAACATCCCAGTCCACCTGAGG   | 1867 |
|  | Db | 1801 | CAAGGCCACAACCATGATGATGCCACAGCAGAGATTTCTTAAACATCCCAGTCCACCTGAGG   | 1860 |
|  | Qy | 1868 | AATGTGTCTCGAATATTTTTCAAAGACTTAAGCCCAAGTGCACTGAAAGTCAAGGCTGGCGCA  | 1927 |
|  | Db | 1861 | AATGTGTCTCGAATATTTTTCAAAGACTTAAGCCCAAGTGCACTGAAAGTCAAGGCTGGCGCA  | 1920 |
|  | Qy | 1928 | CTGTGTCTCTTCCACACAGAGGGCGTGTCTCGGTGCTGACGGGACCCACATGCTCCA        | 1987 |
|  | Db | 1921 | CTGTGTCTCTTCCACACAGAGGGCGTGTCTCGGTGCTGACGGGACCCACATGCTCCA        | 1980 |
|  | Qy | 1988 | GATTAGAGCCTGTAAACTTTATCTATTAACCTTCGATCACCTTAACGGACCAAGCAAGAC     | 2047 |
|  | Db | 1981 | GATTAGAGCCTGTAAACTTTATCTATTAACCTTCGATCACCTTAACGGACCAAGCAAGAC     | 2040 |
|  | Qy | 2048 | CCTAAAACATCATTAATTTGTGTATAGACAGAAACACTATATGMAAGATGAAACCGAGGCTGA  | 2107 |
|  | Db | 2041 | CCTAAAACATCATTAATTTGTGTATAGACAGAAACACTATATGMAAGATGAAACCGAGGCTGA  | 2100 |
|  | Qy | 2108 | GAATCAGACTCAGACGTTTACAGACGCTGCTGTCAACCAAGAAATGTTATGTGCAAGTTT     | 2167 |
|  | Db | 2101 | GAATCAGACTCAGACGTTTACAGACGCTGCTGTCAACCAAGAAATGTTATGTGCAAGTTT     | 2160 |
|  | Qy | 2168 | ATCAGTAAATAACTGGAAAAACAGAACACTTATGTTTATACATACAGATCATCTTGGAACT    | 2227 |
|  | Db | 2161 | ATCAGTAAATAACTGGAAAAACAGAACACTTATGTTTATACATACAGATCATCTTGGAACT    | 2220 |
|  | Qy | 2228 | GCATTTCTTGAGCATGTTTTATATACATGTGTAAATACCCATATGTCTT                | 2276 |
|  | Db | 2221 | GCATTTCTTGAGCATGTTTTATATACATGTGTAAATACCCATATGTCTT                | 2269 |

RESULT 12



Db 721 GATAGAAATAGGGACAAACCTGTTGAA CCAAA CAGCTGAGCAAA CGCGGAAGTTTAAC TGA 780  
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Db 781 TGTGGAAGCCCAAGTATTAAATCAGACCA CAGAGACTTGAAC TTTCACTCTTGGAA CACTC 840  
QY 848 CTTCTCGACAAACAAATTTGGAAAAA CAGATTTTGGACCA GACAGTGAATTA AAAACAAT 907  
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QY 908 GCAAGATAGACAGTTTCTAGAAAAA GAGGTGCTAGCTAT GGAAGACAACCA CATCAT 967  
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QY 968 CCAACTACAGTCAATTAAGAAAGAGAAA GATCAGCTCA GAGTGTAGTATCCAAGCAAAA 1027  
Db 961 CCAACTACAGTCAATTAAGAAAGAGAAA GATCAGCTCA GAGTGTAGTATCCAAGCAAAA 1020  
QY 1028 TTCCATCATTTGAAGAACTAGAAAAA AATAATAGTGA CTGCCACGGTGAATAATTCAGTTCT 1087  
Db 1021 TTCCATCATTTGAAGAACTAGAAAAA AATAATAGTGA CTGCCACGGTGAATAATTCAGTTCT 1080  
QY 1088 TCAAAAGCAGCAACATGATCTCATGGAGACAGT TAATAACTTACTGACTATGATGTCCAC 1147  
Db 1081 TCAAAAGCAGCAACATGATCTCATGGAGACAGT TAATAACTTACTGACTATGATGTCCAC 1140  
QY 1148 ATCAAACCTCAGCTAAGGACCCCACTG TTTGCTTAAAGAA GAAACAAATCAGCTTCAGAGACTG 1207  
Db 1141 ATCAAACCTCAGCTAAGGACCCCACTG TTTGCTTAAAGAA GAAACAAATCAGCTTCAGAGACTG 1200  
QY 1208 TGCTGAAGTATTCAAATCAGGACACACCA CAAATGGCATCTACAGCTTAAACATTCCTTAA 1267  
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QY 1268 TTCTCAGAGAGATCAAGGCTTACTGTGACATGGA CTGGAAGTGGAGGCGGTGACCAAT 1327  
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QY 1508 CTTATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA 1567  
Db 1501 CTTATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA 1560  
QY 1568 AGGACTTACAGGACAGCCGGCAAAATAAGCAGCATCAGCCAA CCAAGGAAATGATTTTAG 1627  
Db 1561 AGGACTTACAGGACAGCCGGCAAAATAAGCAGCATCAGCCAA CCAAGGAAATGATTTTAG 1620  
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Db 1801 CAAAGGCCAACAACATGATCCGACCGACAGATTTCTTAAACAT CCGAGTCCACCTGAGG 1860

QY 1868 AACTGCTCTCGAACTATTTTCAAAGA CTTAAGCCCA GTCGACTGAAAGTCA CGGCTGCGCA 1927  
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QY 1928 CTGTGCTCTCTCCACACAGAGGGCGTGTCTCGGTGCTGACGGGACCCACATGCTCCA 1987  
Db 1921 CTGTGCTCTCTCCACACAGAGGGCGTGTCTCGGTGCTGACGGGACCCACATGCTCCA 1980  
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Db 2221 GCATTTCTTGAGCACTGTTTATACACTGTGTAAATACCCATATGCTCT 2269

## RESULT 13

AR217276

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match

Best Local Similarity

Matches 2269;

Conservative

0; Mismatches

0; Indels

0; Gaps

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QY 68 AGAGAGGAACAAGACCGTGAAGCTGCTGTGTAAGCTGACACAGCCCTCCCAAGTG 127

Db 61 AGAGAGGAACAAGACCGTGAAGCTGCTGTGTAAGCTGACACAGCCCTCCCAAGTG 120

QY 128 AGCAGGACTGTTTCTTCCCACTGCAATCTGACAGTTTACTGTCATGCTGGAGAGAACACAG 187

Db 121 AGCAGGACTGTTTCTTCCCACTGCAATCTGACAGTTTACTGTCATGCTGGAGAGAACACAG 180

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Db 241 CAGCCATGCGACGCTAGCAGCCCTCGCTTTCAGACGGCAGCAGCTCGGACTCTGACGT 300



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## RESULT 14

AR282748  
LOCUS AR282748 2269 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 3 from patent US 6524583.

AR282748  
ACCESSION AR282748

AR282748.1 GI:29719451

KEYWORDS

SOURCE Unknown.

ORGANISM Unclonified.

REFERENCE 1 (bases 1 to 2269)

AUTHORS Thorpe, P.B. and Brekken, R.A.

TITLE Antibody methods for selectively inhibiting VEGF  
JOURNAL Patent: US 6524583-A 3 25-FEB-2003;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 99.4%; Score 2269; DB 6; Length 2269;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
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| QY | 8   | TGGTGTGTTTATCTCTCCAGCCTTGAAGGAGGAAACAACACTGTAGATCTGGG         | 67  |
| DB | 1   | TGGGTGTGTTTATCTCTCCAGCCTTGAAGGAGGAAACAACACTGTAGATCTGGG        | 60  |
| QY | 68  | AGAGAGAACAAAGGACCGTGAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG     | 127 |
| DB | 61  | AGAGAGAACAAAGGACCGTGAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG     | 120 |
| QY | 128 | AGCAGACTGTCTTCCCACTGCAATCTGACAGTTTACTGCAATGCTGAGAGGAAACAAG    | 187 |
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| QY | 188 | CAGTAAAAACAGGTTTGCTACTGGAAGAAAGAGGAAAGAGAGACTTTCATTGACGACC    | 247 |
| DB | 181 | CAGTAAAAACAGGTTTGCTACTGGAAGAAAGAGGAAAGAGAGACTTTCATTGACGACC    | 240 |
| QY | 248 | CAGCATGCGCAGCTAGCAGCCCTGGTTTCAGCGGAGCAGCTCGGACCTCGAGCT        | 307 |
| DB | 241 | CAGCATGCGCAGCTAGCAGCCCTGGTTTCAGCGGAGCAGCTCGGACCTCGAGCT        | 300 |
| QY | 308 | GTGTTTGCCCTCAAGTTTCTAAGCTGCTGGTTTATTAAGTGAAGAAAGAAATGTGCAGAT  | 367 |
| DB | 301 | GTGTTTGCCCTCAAGTTTCTAAGCTGCTGGTTTATTAAGTGAAGAAAGAAATGTGCAGAT  | 360 |
| QY | 368 | TGTTTTCTTTACTGTAGCTGTGATCTGTCTTGGCGGAGCTATAACAATTTCGGAA       | 427 |
| DB | 361 | TGTTTTCTTTACTGTAGCTGTGATCTGTCTTGGCGGAGCTATAACAATTTCGGAA       | 420 |
| QY | 428 | GAGCATGAGACATAGGAAGAAAGCAATATCAGTCCAGCATGGTCTGCGAGCTACAC      | 487 |
| DB | 421 | GAGCATGAGACATAGGAAGAAAGCAATATCAGTCCAGCATGGTCTGCGAGCTACAC      | 480 |
| QY | 488 | TTTCTCTCTGCCAGATGGCAACTGCCGCTCTTCTCCAGCCCTACGTTGCCAATGC       | 547 |
| DB | 481 | TTTCTCTCTGCCAGATGGCAACTGCCGCTCTTCTCCAGCCCTACGTTGCCAATGC       | 540 |
| QY | 548 | TGTGAGAGGAGCGCGCTCGAATACGATGACTCGGTGAGAGCTGCAAGTGTGGA         | 607 |
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| QY | 608 | GAACATCATGGAAGAAACAACACTCAGTGGCTAATGAAGCTTGAGAAATATATCCAGACAA | 667 |
| DB | 601 | GAACATCATGGAAGAAACAACACTCAGTGGCTAATGAAGCTTGAGAAATATATCCAGACAA | 660 |
| QY | 668 | CATGAAGAAAGAAATGGTAGATACAGCAGAAATGCAGTACAGAACCCAGCGCTGTGAT    | 727 |
| DB | 661 | CATGAAGAAAGAAATGGTAGATACAGCAGAAATGCAGTACAGAACCCAGCGCTGTGAT    | 720 |
| QY | 728 | GATGAATATAGGACAAACCTGTGAACCAACAGCTGAGGCAACCCGGAAGTTAATCTGA    | 787 |
| DB | 721 | GATGAATATAGGACAAACCTGTGTAAACCAACAGCTGAGGCAACCCGGAAGTTAATCTGA  | 780 |
| QY | 788 | TGTGAAGCCCAAGTATTAAATCAGACCAAGACTTGAACCTTCAGCTCTTGGAAACACTC   | 847 |
| DB | 781 | TGTGAAGCCCAAGTATTAAATCAGACCAAGACTTGAACCTTCAGCTCTTGGAAACACTC   | 840 |
| QY | 848 | CCTCTCGACAAACAAATTTGGAAGAAACAGATTTTGGACCAAGCAGTGAATATAACAAAT  | 907 |
| DB | 841 | CCTCTCGACAAACAAATTTGGAAGAAACAGATTTTGGACCAAGCAGTGAATATAACAAAT  | 900 |
| QY | 908 | GCAAGATAAGACAGTTTCTAGAAAAAGAGTGTAGCTATGGAAGACAGCATCAT         | 967 |

|    |      |   |      |
|----|------|---|------|
| DB | 901  | GCAAGATAAGAACAGTTTCTAGAAAAAGAGGTGTAGCTATGGAAGACAAAGCATCAT     | 960  |
| QY | 968  | CCAACTACAGTCAATAAAGAGAGAGAGATCAGCTCAGAGTGTAGTATCAAGCAAAA      | 1027 |
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| QY | 1028 | TTCCATCATTTGAAGAACTAGAAAAAAAATAGTGTCCACGCGTGAATAATTCAGTTCT    | 1087 |
| DB | 1021 | TTCCATCATTTGAAGAACTAGAAAAAAAATAGTGTCCACGCGTGAATAATTCAGTTCT    | 1080 |
| QY | 1088 | TCAAAAGCAGCAACATGATCTCATGAGACAGTTTAACTTACTGACTATGATGTCCAC     | 1147 |
| DB | 1081 | TCAAAAGCAGCAACATGATCTCATGAGACAGTTTAACTTACTGACTATGATGTCCAC     | 1140 |
| QY | 1148 | ATCAAACTCAGCTAAGGACCCACCTGTTCTAAAGAAACAAATCAGCTTCAGAGACTG     | 1207 |
| DB | 1141 | ATCAAACTCAGCTAAGGACCCACCTGTTCTAAAGAAACAAATCAGCTTCAGAGACTG     | 1200 |
| QY | 1208 | TGCTGAAGTATTCAAAATCAGGACACACCAAAATGGCATCTACAGTTTAACTTCCCTAA   | 1267 |
| DB | 1201 | TGCTGAAGTATTCAAAATCAGGACACACCAAAATGGCATCTACAGTTTAACTTCCCTAA   | 1260 |
| QY | 1268 | TTCTACAGAAAGATCAAGGCTACTGTGACATGGAAGCTGGAGAGCGGTGGACAA        | 1327 |
| DB | 1261 | TTCTACAGAAAGATCAAGGCTACTGTGACATGGAAGCTGGAGAGCGGTGGACAA        | 1320 |
| QY | 1328 | TATTCAGCGACGTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGAAATAAAGT   | 1387 |
| DB | 1321 | TATTCAGCGACGTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGAAATAAAGT   | 1380 |
| QY | 1388 | GGGATTTGGTAAACCTTCAGGAGAAATATGGCTGGGAAATGAGTTTGTTCGCAATGCAC   | 1447 |
| DB | 1381 | GGGATTTGGTAAACCTTCAGGAGAAATATGGCTGGGAAATGAGTTTGTTCGCAATGCAC   | 1440 |
| QY | 1448 | TAACTCAGCAACGCTATGCTTTAAATAACACCTTAAAGACTGGGAGGAAATGAGCTTA    | 1507 |
| DB | 1441 | TAACTCAGCAACGCTATGCTTTAAATAACACCTTAAAGACTGGGAGGAAATGAGCTTA    | 1500 |
| QY | 1508 | CTCATTTGATGAACATTTCTATCTCAAGTGAAGAACTCAATATAGGATTCACCTTAA     | 1567 |
| DB | 1501 | CTCATTTGATGAACATTTCTATCTCAAGTGAAGAACTCAATATAGGATTCACCTTAA     | 1560 |
| QY | 1568 | AGGACTTACAGGACAGCGGCAAAATAGCAGCATCAGCCAAACAGGAAATGATTTAG      | 1627 |
| DB | 1561 | AGGACTTACAGGACAGCGGCAAAATAGCAGCATCAGCCAAACAGGAAATGATTTAG      | 1620 |
| QY | 1628 | CACAAAGATGGAGACAGCAAAATGATTTGCAAAATGTTTCAAAATGCTTAACAGGAGG    | 1687 |
| DB | 1621 | CACAAAGATGGAGACAGCAAAATGATTTGCAAAATGTTTCAAAATGCTTAACAGGAGG    | 1680 |
| QY | 1688 | CTGGTGGTTTGATGATGCTGCTTCCAACTTGAAACGGAATGTACTATCCACAGAGCA     | 1747 |
| DB | 1681 | CTGGTGGTTTGATGATGCTGCTTCCAACTTGAAACGGAATGTACTATCCACAGAGCA     | 1740 |
| QY | 1748 | GAACAAATAGTTTCAACGCGATTTAAATGCTTACTTGGAAAGGCTCAGGCTATTCGCT    | 1807 |
| DB | 1741 | GAACAAATAGTTTCAACGCGATTTAAATGCTTACTTGGAAAGGCTCAGGCTATTCGCT    | 1800 |
| QY | 1808 | CAAGGCCAACCAATGATGATCGGACAGCAGATTTCTTAAACATCCAGTCCACCTGAGG    | 1867 |
| DB | 1801 | CAAGGCCAACCAATGATGATCGGACAGCAGATTTCTTAAACATCCAGTCCACCTGAGG    | 1860 |
| QY | 1868 | AATGTCTCGAACTATTTTCAAGACTTTAAGCCAGTGCATCTGAAAGTCAACGGCTGCGCA  | 1927 |
| DB | 1861 | AATGTCTCGAACTATTTTCAAGACTTTAAGCCAGTGCATCTGAAAGTCAACGGCTGCGCA  | 1920 |
| QY | 1928 | CTGTGCTCTTCCACCAAGAGGCGGTGTGCTCGGTGCTGACGCGGACCCACATGCTCCA    | 1987 |
| DB | 1921 | CTGTGCTCTTCCACCAAGAGGCGGTGTGCTCGGTGCTGACGCGGACCCACATGCTCCA    | 1980 |
| QY | 1988 | GATTAGAGCTGTAACTTTTATCACTTAAACCTTGATCACTTAAACGCGGACCAAGCAAGAC | 2047 |

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Qy 2168 ATCAGTAAATAAATCGGAACACAAACATTTATGTTATACAAATACAGATCATCTTGGAACT 2227

Db 2161 ATCAGTAAATAAATCGGAACACAAACATTTATGTTATACAAATACAGATCATCTTGGAACT 2220

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Db 2221 GCATTTCTTCTGAGCACTGTTTATACACTGTGTAAATACCAATATGTCCT 2269

RESULT 15

AR451799

LOCUS AR451799 2269 bp DNA linear PAT 20-FEB-2004

DEFINITION Sequence 3 from patent US 6676941.

ACCESSION AR451799

VERSION AR451799.1 GI:42682922

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2269)

AUTHORS Thorpe, P. E. and Brekken, R. A.

TITLE Antibody conjugate formulations for selectively inhibiting VEGF

JOURNAL Patent: US 6676941-A 3 13-JAN-2004;

FEATURES

Location/Qualifiers

1..2269

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match 99.4%; Score 2269; DB 6; Length 2269;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TGGTTGGTGTATCTCTCCAGCCTTGAGGAGGAGAAACACCTGTAGGATCTGGGG 67

Db 1 TGGTTGGTGTATCTCTCTCCAGCCTTGAGGAGGAGAAACACCTGTAGGATCTGGGG 60

Qy 68 AGAGAGGAACAAGGACCGTGAAGCTGCTGTGTAAGCTGACACAGCCCTCCCAAGTG 127

Db 61 AGAGAGGAACAAGGACCGTGAAGCTGCTGTGTAAGCTGACACAGCCCTCCCAAGTG 120

Qy 128 AGCAGGACTGTTCTCCAGCTGCAATCTGACAGTTTACTGCATGCCCTGGAGAGAACAG 187

Db 121 AGCAGGACTGTTCTCCAGCTGCAATCTGACAGTTTACTGCATGCCCTGGAGAGAACAG 180

Qy 188 CAGTAAACACAGGTTTGTCTACTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 247

Db 181 CAGTAAACACAGGTTTGTCTACTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

Qy 248 CAGCCATGGCAGCGTAGCAGCCCTCGCGTTTCAGACGGCAGCAGCTCGGAGCTCTGGACGT 307

Db 241 CAGCCATGGCAGCGTAGCAGCCCTCGCGTTTCAGACGGCAGCAGCTCGGAGCTCTGGACGT 300

Qy 308 GTGTTTGGCCCTCAAGTTTGTAAAGCTGCTGTTTATCTGAGAGAAAGATGTGGCAGAT 367

Db 301 GTGTTTGGCCCTCAAGTTTGTAAAGCTGCTGTTTATCTGAGAGAAAGATGTGGCAGAT 360

Qy 368 TGTTTCTTTTACTCTGAGCTGTGATCTGTCTGCGCGCAGCCTATACAACTTTCGAA 427

Db 361 TGTTTCTTTTACTCTGAGCTGTGATCTGTCTGCGCGCAGCCTATACAACTTTCGAA 420

Qy 428 GAGCATGGACAGCATAGGAAGAGCAATATCAGGTCCAGCATGGGTCTCGACTACAC 487

Db 421 GAGCATGGACAGCATAGGAAGAAAGCAATATCAGGTCCAGCATGGGTCTCGAGCTACAC 480

Qy 488 TTTCTCTCTCCAGAGATGGAACAACTGCGCTCTTCTCTCAGCCCCCTACGTGTCCAAATGC 547

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Db 601 GAACATCATCTGGAACAAACAACTCAGTGGCTTAATGAAGCTTGAATATATCCAGACAA 660

Qy 668 CATGAAGAAAGAAATGTTAGAGATACAGAGAAATGCAAGTACAGAACAGACGCTGTGAT 727

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Db 961 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTAGTATCCAAAGCAAAA 1020

Qy 1028 TTCCATCATTTGAAGAACTAGAAACCAATAGTGAATGCTGACCGTGAATAATTCAGTTCT 1087

Db 1021 TTCCATCATTTGAAGAACTAGAAACCAATAGTGAATGCTGACCGTGAATAATTCAGTTCT 1080

Qy 1088 TCAAAAGCAGCAACATGATCTCATGAGACAGTTAATTAATCTTACTGATGATGTCAC 1147

Db 1081 TCAAAAGCAGCAACATGATCTCATGAGACAGTTAATTAATCTTACTGATGATGTCAC 1140

Qy 1148 ATCAAACTCAGCTAAGGACCCCACTGTGTCTAAAGAGAAACAAATCAGCTTCAGAGACTG 1207

Db 1141 ATCAAACTCAGCTAAGGACCCCACTGTGTCTAAAGAGAAACAAATCAGCTTCAGAGACTG 1200

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Qy 1268 TTCTACAGAGAGATCAAGGCCCTACTGTGACATGGAAGCTTGGAGAGCGGGTGGACAAT 1327

Db 1261 TTCTACAGAGAGATCAAGGCCCTACTGTGACATGGAAGCTTGGAGAGCGGGTGGACAAT 1320

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Qy 1388 GGGATTTGGTAAACCTTTTCAGGAGAAATTTGGCTGGGAAATGAGTTTTCGCAACTGAC 1447

Db 1381 GGGATTTGGTAAACCTTTTCAGGAGAAATTTGGCTGGGAAATGAGTTTTCGCAACTGAC 1440

Qy 1448 TAATCAGCAACCGTATGTGCTTAAATAACCTTTAAAGA CTGGGAAGGGAATGAGGCTTA 1507

Db 1441 TAATCAGCAACCGTATGTGCTTAAATAACCTTTAAAGA CTGGGAAGGGAATGAGGCTTA 1500

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QY 1568 AGGACTTACAGGACAGCCGGCAAAATAGCAGCATCAGCCAAACAGGAAATGATTTTAG 1627
Db |||||||
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Db |||||||
1861 AACTGTCTCGAACTATTTTCAAAGACTTAAAGCCAGTGCACCTGAAAGTCAAGGCTGCGCA 1920
QY 1928 CTGTGTCTCTTCCACCAAGAGGGGCTGTGCTCGTGTGACGGGACCCACATGCTCCA 1987
Db |||||||
1921 CTGTGTCTCTTCCACCAAGAGGGGCTGTGCTCGTGTGACGGGACCCACATGCTCCA 1980
QY 1988 GATTAGAGCCTGTAAACCTTTATCATTAACTTTGATGCAATGCTTAAACGGACCAAGCAAGAC 2047
Db |||||||
1981 GATTAGAGCCTGTAAACCTTTATCATTAACTTTGATGCAATGCTTAAACGGACCAAGCAAGAC 2040
QY 2048 CCTAAACATCCATAATTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA 2107
Db |||||||
2041 CCTAAACATCCATAATTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA 2100
QY 2108 GAATCAGACTGACAGTTTACAGACGCTGCTGTACAAACCAAGAAATGTTATGTGCAAGTTT 2167
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2101 GAATCAGACTGACAGTTTACAGACGCTGCTGTACAAACCAAGAAATGTTATGTGCAAGTTT 2160
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Search completed: July 29, 2005, 06:57:13  
Job time : 10198.7 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 00:20:09 ; Search time 1301.44 Seconds  
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10379.917 Million cell updates/sec

Title: US-10-603-293-5  
Perfect score: 2282  
Sequence: 1 gaattcctgggtggtgttt.....taccatattgctctgaattc 2282

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
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- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 4          | 2269   | 99.4        | 2269   | 3 AAZ92215  | Aaz92215 Human ang  |
| 5          | 2269   | 99.4        | 2269   | 3 AAZ92213  | Aaz92213 Human ang  |
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| 7          | 2269   | 99.4        | 2269   | 5 AAS70958  | Aas70958 DNA encod  |
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| 9          | 2269   | 99.4        | 2269   | 6 ABK47716  | Abk47716 DNA encod  |
| 10         | 2269   | 99.4        | 2269   | 8 ABX12556  | Abx12556 cDNA encod |
| 11         | 2269   | 99.4        | 2269   | 11 ADN95380 | Adn95380 Human BEC  |
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|----|--------|------|--------|-------------|--------------------|
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| 22 | 1290.6 | 56.6 | 1500   | 2 AAV18616  | Aav18616 Nucleotid |
| 23 | 1210   | 53.0 | 1376   | 6 ABK10923  | Abk10923 Gene enco |
| 24 | 1210   | 53.0 | 1376   | 12 ADQ09387 | Adq09387 Human ang |
| 25 | 1186.6 | 52.0 | 1387   | 8 AAD49987  | Aad49987 Human ang |
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| 38 | 595.6  | 26.1 | 240823 | 10 ADD69391 | Add69391 Human PG- |
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| 42 | 551.6  | 24.2 | 2146   | 2 AAT14649  | Aat14649 Human TIE |
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| 45 | 550.2  | 24.1 | 1494   | 9 AAD58428  | Aad58428 Human ang |

ALIGNMENTS

RESULT 1  
AAT14650

ID: AAT14650 standard; DNA; 2282 BP.

XX AAT14650;

DT 28-OCT-1996 (first entry)

Human TIE-2 ligand 2-encoding DNA derived from pBluescript KS clone.

Angiogenesis; neovascularisation; tumour development; wound healing; TIE;  
tyrosine kinase with Ig and EGF homology domains; vector; recombinant;  
clone; diagnosis; ischaemia; thromboembolytic disease; atherosclerosis;  
inflammation; diabetes; ligand bodies; delivery; targeting; ss.

OS Homo sapiens.

XX Key Location/Qualifiers  
FT CDS 357..1847  
FT /\*tag= a

PN WO9611269-A2.

PD 18-APR-1996.

XX 06-OCT-1995; 95WO-US012935.

XX 07-OCT-1994; 94US-00319932.

XX 27-OCT-1994; 94US-00330261.

XX 02-DEC-1994; 94US-00348492.

XX 09-DEC-1994; 94US-00353503.

XX 17-JAN-1995; 95US-00373579.

XX 06-APR-1995; 95US-00418595.

XX (REG-) REGENERON PHARM INC.

XX Davis S, Bruno J, Goldfarb M, Aldrich TH, Maisompierre PC;  
PI Radzilewski C, Jones PF, Yancopoulos GD;

XX WPI; 1996-209850/21.

XX P-PSDB; AAR94605.

XX Nucleic acid encoding TIE-2 ligand and related vectors - useful in





Db 1801 ATTGCTCAAGGCCACAACCATGATGATCGGACGACAGATTCTTAAACATCCAGTCCA 1860  
QY 1861 CTTGAGGAACGTCTCGAACTATTTTCAAGACTTAAGCCAGTGCAGCTGAAGTCAACGG 1920  
Db 1861 CTTGAGGAACGTCTCGAACTATTTTCAAGACTTAAGCCAGTGCAGCTGAAGTCAACGG 1920  
QY 1921 CTTGAGGAACGTCTCGAACTATTTTCAAGACTTAAGCCAGTGCAGCTGAAGTCAACGG 1980  
Db 1921 CTTGAGGAACGTCTCGAACTATTTTCAAGACTTAAGCCAGTGCAGCTGAAGTCAACGG 1980  
QY 1981 TGGCTCAGATAGAGCTGTAACTTTATCATTAACTTTGACATCACTTAAACCGGACCAA 2040  
Db 1981 TGGCTCAGATAGAGCTGTAACTTTATCATTAACTTTGACATCACTTAAACCGGACCAA 2040  
QY 2041 GCAAGACCCCTAAACATCCATAATTGATTAGACAGAACACCTATGCAAGATGAACCCG 2100  
Db 2041 GCAAGACCCCTAAACATCCATAATTGATTAGACAGAACACCTATGCAAGATGAACCCG 2100  
QY 2101 AGGCTGAGATCAGATGACAGTTTACAGACGCTGTGTACAAACCAAGATGTTATGTG 2160  
Db 2101 AGGCTGAGATCAGATGACAGTTTACAGACGCTGTGTACAAACCAAGATGTTATGTG 2160  
QY 2161 CAAGTTTATCAGTAATACTGGAACACAGAACTATGTTATACATACATACATCATCT 2220  
Db 2161 CAAGTTTATCAGTAATACTGGAACACAGAACTATGTTATACATACATACATCATCT 2220  
QY 2221 TGGAACTGCACTTCTTGAGCAGCTGTTTATACACTGTGTAAATACCCATATGTCCTGAAT 2280  
Db 2221 TGGAACTGCACTTCTTGAGCAGCTGTTTATACACTGTGTAAATACCCATATGTCCTGAAT 2280  
QY 2281 TC 2282  
Db 2281 TC 2282

RESULT 2  
AAT44321  
ID AAT44321 standard; cdna; 2282 BP.  
AC AAT44321;  
XX 11-FEB-1997 (first entry)  
XX Human TIE-2 ligand 2 cdna clone.  
XX TIE-2 ligand 2; tyrosine kinase with Ig and EGF homology domain;  
KW receptor; antagonist; neovascularisation; wound healing; ischaemia;  
KW leukopaenia; thrombocytopaenia; anaemia; angiogenesis; tumour;  
KW atherosclerosis; inflammation; diagnosis; therapy; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 357..1847  
FT CDS /\*tag= a  
XX  
XX WO9631598-A1.  
XX 10-OCT-1996.  
XX  
XX 05-APR-1996; 96WO-US004806.  
XX  
XX 06-APR-1995; 95US-00418595.  
PR 06-OCT-1995; 95WO-US012935.  
XX  
XX (REGE-) REGENERON PHARM INC.  
XX Davis S, Bruno J, Goldfarb M, Aldrich TH, Maisonnier PC;  
PI Radziejewski C, Jones PF, Yancopoulos GD;  
XX WPI; 1996-465021/46.  
DR P-PSDB; AAW01411.  
XX

PT TIE-2 agonists and antagonists and related DNA - useful for promoting or  
PT blocking neovascularisation, etc.  
PS Claim 4; Fig 6; 113pp; English.  
XX A cdna clone (AAT44321) codes for a human TIE-2 (tyrosine kinase with Ig  
CC and EGF homology domains) ligand 2 (AAW01411) that binds the TIE-2  
CC receptor. It was obtd. by screening a human foetal lung cDNA library in  
CC lambda gt10 with a human TIE-2 ligand 1 (see also AAT44319) sequence. TIE  
CC -2 ligand 2 is a receptor antagonist useful for blocking blood vessel  
CC growth, for tumour therapy and for treating a proliferative disorder of a  
CC blood-forming organ. The cdna clone can be used to produce recombinant  
CC TIE-2 ligand in transformed host cells  
SQ Sequence 2282 BP; 746 A; 498 C; 520 G; 518 T; 0 U; 0 Other;  
Query Match 100.0%; Score 2282; DB 2; Length 2282;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAATTCCTGGTGTGGTGTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGA 60  
Db 1 GAATTCCTGGTGTGGTGTATCTCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGA 60  
QY 61 TCTGGGAGAGAGGAAACAAGGACCTGAAAGCTGCTGTAAAGCTGCACAGCCCTC 120  
Db 61 TCTGGGAGAGAGGAAACAAGGACCTGAAAGCTGCTGTAAAGCTGCACAGCCCTC 120  
QY 121 CCAAGTGAGCAGACACTGTTCTTCCCACTGCAATCTGACAGCTTTACTGTCATGCGAGAG 180  
Db 121 CCAAGTGAGCAGACACTGTTCTTCCCACTGCAATCTGACAGCTTTACTGTCATGCGAGAG 180  
QY 181 AACACAGCAGTAAAAAACCAAGTTTGTCTAAGCTGCTGGTTTATTACTGAAGAAAGATGT 240  
Db 181 AACACAGCAGTAAAAAACCAAGTTTGTCTAAGCTGCTGGTTTATTACTGAAGAAAGATGT 240  
QY 241 ACGGACCCAGCCTGAGCGGTAGCAGCCTGCTTTCAGACGCGCAGCAGCTCGGACTC 300  
Db 241 ACGGACCCAGCCTGAGCGGTAGCAGCCTGCTTTCAGACGCGCAGCAGCTCGGACTC 300  
QY 301 TGGACGTGTGTTGGCCCTCAAGTTTGTCTAAGCTGCTGGTTTATTACTGAAGAAAGATGT 360  
Db 301 TGGACGTGTGTTGGCCCTCAAGTTTGTCTAAGCTGCTGGTTTATTACTGAAGAAAGATGT 360  
QY 361 GGCAGATGTTTCTTTTACTCTGAGCTGTGATCTTGTCTTGGCGGAGCCTATTAACAAT 420  
Db 361 GGCAGATGTTTCTTTTACTCTGAGCTGTGATCTTGTCTTGGCGGAGCCTATTAACAAT 420  
QY 421 TTCGGAAGAGCATGGACAGCATAGGAAGAAGCAATATCAGTCCAGCATGGTCTCTGCA 480  
Db 421 TTCGGAAGAGCATGGACAGCATAGGAAGAAGCAATATCAGTCCAGCATGGTCTCTGCA 480  
QY 481 GCTACACTTTCCTCTCCAGAGATGACAACTGCGCTCTTCTCCAGCCCTTACCTGT 540  
Db 481 GCTACACTTTCCTCTCCAGAGATGACAACTGCGCTCTTCTCCAGCCCTTACCTGT 540  
QY 541 CCAATGCTGTGCAGAGGAGCGCGCTCGAATACGATGACTCGGTGCAGAGGCTGCAAG 600  
Db 541 CCAATGCTGTGCAGAGGAGCGCGCTCGAATACGATGACTCGGTGCAGAGGCTGCAAG 600  
QY 601 TGTGGAGAAACATCATGGAAAAAACAACCTCAGTGGCTTAAGAGCTTGAGAAATATATCC 660  
Db 601 TGTGGAGAAACATCATGGAAAAAACAACCTCAGTGGCTTAAGAGCTTGAGAAATATATCC 660  
QY 661 AGGACACATGAAAGAAAGAAATGTTAGATACAGCAGAAATGCAATACAGAACACGACGG 720  
Db 661 AGGACACATGAAAGAAAGAAATGTTAGATACAGCAGAAATGCAATACAGAACACGACGG 720  
QY 721 CTGTGATGATAGAAATAGGACAAACCTGTTTGAACCAACAGCTGAGCAAAACGCGGAAGT 780  
Db 721 CTGTGATGATAGAAATAGGACAAACCTGTTTGAACCAACAGCTGAGCAAAACGCGGAAGT 780  
QY 781 TAACTGATGTGGAGAGCCCAAGTATTAAATCAGACACGAGACTTGAACCTTCCTGG 840

Db 781 |||||TAACTGATGTGGAAGCCCAAGTATTAAATCAGACCAAGAGACTTGAACTTCAGCTCTTGG 840  
Qy 841 AACACTCCCTCTCGCAAAACAAATTTGGAAAAACAGATTTTGGACCAAGACAGTGAATAA 900  
Db 841 AACACTCCCTCTCGCAAAACAAATTTGGAAAAACAGATTTTGGACCAAGACAGTGAATAA 900  
Qy 901 ACAAAATTGCAAGATAAGAACAGTTTCTTAGAAAAAGAGGTGTAGCTATGGAAGACAAGC 960  
Db 901 ACAAAATTGCAAGATAAGAACAGTTTCTTAGAAAAAGAGGTGTAGCTATGGAAGACAAGC 960  
Qy 961 ACATCATCAACTCAGTCAATTAAGAAAGAGAAAGATCAGCTACAGGTGTAGTATCCA 1020  
Db 961 ACATCATCAACTCAGTCAATTAAGAAAGAGAAAGATCAGCTACAGGTGTAGTATCCA 1020  
Qy 1021 AGCAAAATTCATTTGAAGAACTAGAAAAAATAATAGTGTGCTGCAAGGTGAATAATT 1080  
Db 1021 AGCAAAATTCATTTGAAGAACTAGAAAAAATAATAGTGTGCTGCAAGGTGAATAATT 1080  
Qy 1081 CAGTTCTTCAAAAGCAGCAACATGATCTCATGGAGACAGTTAATACTTACTGACTATGA 1140  
Db 1081 CAGTTCTTCAAAAGCAGCAACATGATCTCATGGAGACAGTTAATACTTACTGACTATGA 1140  
Qy 1141 TGTCCACATCAACTCAGCTAAGGACCCCACTGTTGCTTAAGAGAAACAAATCAGCTTCA 1200  
Db 1141 TGTCCACATCAACTCAGCTAAGGACCCCACTGTTGCTTAAGAGAAACAAATCAGCTTCA 1200  
Qy 1201 GAGACTGTCTGAAGTATTCAAATCAGGACACACACAATGSCATCTACAGTTAAACAT 1260  
Db 1201 GAGACTGTCTGAAGTATTCAAATCAGGACACACACAATGSCATCTACAGTTAAACAT 1260  
Qy 1261 TCCCTAAATCTACAGAAGAGATCAAGGCCTACTGTGACATGGAAGCTGGAGAGCGGCT 1320  
Db 1261 TCCCTAAATCTACAGAAGAGATCAAGGCCTACTGTGACATGGAAGCTGGAGAGCGGCT 1320  
Qy 1321 GGACAAATTTACAGCA COTGAGAGATGGCAGCGTTGA TTTTCAGAGGACTTGGAAAGAAAT 1380  
Db 1321 GGACAAATTTACAGCA COTGAGAGATGGCAGCGTTGA TTTTCAGAGGACTTGGAAAGAAAT 1380  
Qy 1381 ATAAAGTGGGATTTGTGTAACCTTCAGGAGAAATATTTGGCTGGGAAATGATTTTTCGC 1440  
Db 1381 ATAAAGTGGGATTTGTGTAACCTTCAGGAGAAATATTTGGCTGGGAAATGATTTTTCGC 1440  
Qy 1441 AACTGACTAATCAGCAACGCTATGTCTTAAATAACACCTTAAAGACTTGGGAAAGGAAATG 1500  
Db 1441 AACTGACTAATCAGCAACGCTATGTCTTAAATAACACCTTAAAGACTTGGGAAAGGAAATG 1500  
Qy 1501 AGGCTTACTCATTTGTAACATTTCTATCTCAAGTGAAGAACTCAATTTATAGATTC 1560  
Db 1501 AGGCTTACTCATTTGTAACATTTCTATCTCAAGTGAAGAACTCAATTTATAGATTC 1560  
Qy 1561 ACCTTAAAGGACTTACAGGACAGCGGCAAAATAAGCAGCATCAGCCAAACAGGAAATG 1620  
Db 1561 ACCTTAAAGGACTTACAGGACAGCGGCAAAATAAGCAGCATCAGCCAAACAGGAAATG 1620  
Qy 1621 ATTTTAGCAAAAGGATGGAGACAACGAAATGATTTTGCAAAATGTTTCAAAAATGCTAA 1680  
Db 1621 ATTTTAGCAAAAGGATGGAGACAACGAAATGATTTTGCAAAATGTTTCAAAAATGCTAA 1680  
Qy 1681 CAGGAGGCTGGTGGTGTGATGATGTGCTTCCAACTTGAACGGAATGTACTATCCAC 1740  
Db 1681 CAGGAGGCTGGTGGTGTGATGATGTGCTTCCAACTTGAACGGAATGTACTATCCAC 1740  
Qy 1741 AGAGGCAGAAACAAATTAAGTTCAACGGCATTTAAATGGTACTTCTGGAAGGCTCAGGCT 1800  
Db 1741 AGAGGCAGAAACAAATTAAGTTCAACGGCATTTAAATGGTACTTCTGGAAGGCTCAGGCT 1800  
Qy 1801 ATTGCTCAAGGCCCAACACCATGATGATCCGACGAGATTTCTTAAACATCCCAAGTCCA 1860  
Db 1801 ATTGCTCAAGGCCCAACACCATGATGATCCGACGAGATTTCTTAAACATCCCAAGTCCA 1860  
Qy 1861 CTTGAGGAGACTGTCTGCACTATTTTCAAGACTTAAGCCGAGTCACTGAAGTCAAGG 1920

Db 1861 CTTGAGGAACTGTCTCGAACTATTTTCAAGACTATTAAGCCAGTGCATCTGAAAGTCACGG 1920  
Qy 1921 CTGCGCACTGTCTCTCTCTTTCCACCACAGAGGCGGTGTCTCGTGTGACGGGACCCACA 1980  
Db 1921 CTGCGCACTGTCTCTCTCTTTCCACCACAGAGGCGGTGTCTCGTGTGACGGGACCCACA 1980  
Qy 1981 TGCTCCAGATTAGAGCCCTGTAAACTTTTATCACTTAAACTTTGCATCACTTAAACGGACCAA 2040  
Db 1981 TGCTCCAGATTAGAGCCCTGTAAACTTTTATCACTTAAACTTTGCATCACTTAAACGGACCAA 2040  
Qy 2041 GCAAGACCCCTAAACATCAATTTGTGATTAGACAGAACACCTATGCAAGAGATGAACCG 2100  
Db 2041 GCAAGACCCCTAAACATCAATTTGTGATTAGACAGAACACCTATGCAAGAGATGAACCG 2100  
Qy 2101 AGGCTGAGAATCAGACTGACAGTTTTACAGAGCTGTGTCAAACTGTGTATGTG 2160  
Db 2101 AGGCTGAGAATCAGACTGACAGTTTTACAGAGCTGTGTCAAACTGTGTATGTG 2160  
Qy 2161 CAAAGTTTATCAGTAAATAAATCTGAAAAACAGAACACTTATGTTATACAAATCAGATCATCT 2220  
Db 2161 CAAAGTTTATCAGTAAATAAATCTGAAAAACAGAACACTTATGTTATACAAATCAGATCATCT 2220  
Qy 2221 TGGAACTGCATTTCTTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGCTCTGAAT 2280  
Db 2221 TGGAACTGCATTTCTTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGCTCTGAAT 2280  
Qy 2281 TC 2282  
Db 2281 TC 2282

RESULT 3  
AAV18619  
ID AAV18619 standard; DNA; 2282 BP.  
XX AAV18619;  
AC AAV18619;  
XX 09-SEP-1998 (first entry)  
XX Human TIE-2 ligand 2 from clone pBluescript KS.  
DE Chimeric TIE ligand 2N1C1F; TIE-2 ligand; neovascularisation; tumour;  
KW human; ss.  
XX Homo sapiens.  
OS Homo sapiens.  
FH Key  
CDS 357..1847  
FT /\*tag= a  
FT /note= "human TIE-2 ligand 2"  
XX  
XX WO9805779-A1.  
XX  
XX 12-FEB-1998.  
XX  
XX 01-AUG-1997; 97WO-US013557.  
XX  
XX 02-AUG-1996; 96US-0022999p.  
XX 25-OCT-1996; 96US-00740223.  
XX (REG- ) REGENERON PHARM INC.  
XX  
XX Davis S, Yancopoulos GD;  
XX  
XX WPI; 1998-145615/13.  
XX P-PSDB; AAW47532.  
XX  
XX Modified human TIE-2 receptor ligand(s) - useful for promoting wound healing.  
XX  
XX Example 8; Fig 6; 202pp; English.  
XX  
XX This is the nucleotide sequence of the human TIE-2 ligand 2, used in the

CC method of the invention, involving the production of TIE-2 ligands which  
CC promote healing. The nucleic acids, vectors and host cells used in the  
CC method of the invention are useful for the recombinant production of the  
CC ligands. The ligands, etc. are useful for blocking blood vessel growth,  
CC promoting neovascularisation, promoting the growth or differentiation of  
CC a cell expressing the TIE receptor, blocking the growth or  
CC differentiation of a cell expressing the TIE receptor and for attenuating  
CC or preventing tumour growth in a human  
XX  
SQ Sequence 2282 BP; 746 A; 497 C; 520 G; 519 T; 0 U; 0 Other;  
  
Query Match 99.9%; Score 2280.4; DB 2; Length 2282;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GAATTCCTGGGTTGGTGTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGA 60  
DB 1 GAATTCCTGGGTTGGTGTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGA 60  
  
QY 61 TCTGGGAGAGAGAAACAAGGACCGTGAAGCTGCTCTGTAAAGCTGACACAGCCCTC 120  
DB 61 TCTGGGAGAGAGAAACAAGGACCGTGAAGCTGCTCTGTAAAGCTGACACAGCCCTC 120  
  
QY 121 CCAAGTCAGCAGACTGTTCTTCCACTGCAATCTGACGTTTACTGTCATGCCCTGGAG 180  
DB 121 CCAAGTCAGCAGACTGTTCTTCCACTGCAATCTGACGTTTACTGTCATGCCCTGGAG 180  
  
QY 181 AACACAGCAGTAAACCCAGCTTGTCTGAAAAGAGGAAAGAGAACTTTCATTG 240  
DB 181 AACACAGCAGTAAACCCAGCTTGTCTGAAAAGAGGAAAGAGAACTTTCATTG 240  
  
QY 241 ACGGACCCAGCCTAGCGGTAGCAGCCCTGCGTTCAGACGCGCAGCAGCTCGGACTC 300  
DB 241 ACGGACCCAGCCTAGCGGTAGCAGCCCTGCGTTCAGACGCGCAGCAGCTCGGACTC 300  
  
QY 301 TGAACGTGTGTCCTCAAGTTTGTCTGAAAGTGTCTGTTTATCTGAAAGAAAGATGT 360  
DB 301 TGAACGTGTGTCCTCAAGTTTGTCTGAAAGTGTCTGTTTATCTGAAAGAAAGATGT 360  
  
QY 361 GGCAGATGTTCTTACTCTGAGCTGTATCTTGTGGCGCAGCCTATTAACAAT 420  
DB 361 GGCAGATGTTCTTACTCTGAGCTGTATCTTGTGGCGCAGCCTATTAACAAT 420  
  
QY 421 TTCCGAAGAGCATGGAACAGATAGGAAGCAATATCAGTTCAGCATGGGTCTGCA 480  
DB 421 TTCCGAAGAGCATGGAACAGATAGGAAGCAATATCAGTTCAGCATGGGTCTGCA 480  
  
QY 481 GCTACACTTCTCTCCAGAGATGGAACACTGCGCTCTTCTCCAGCCCTTACGTGT 540  
DB 481 GCTACACTTCTCTCCAGAGATGGAACACTGCGCTCTTCTCCAGCCCTTACGTGT 540  
  
QY 541 CCAATGCTGTGAGAGGAGCGCGCTCGAATACGATGACTCGGTGCAGAGGCTGCAAG 600  
DB 541 CCAATGCTGTGAGAGGAGCGCGCTCGAATACGATGACTCGGTGCAGAGGCTGCAAG 600  
  
QY 601 TGCTGGAGAACATCATGGAACAACTCACTGAGTGTAAAGCTTTCAGAAATATATCC 660  
DB 601 TGCTGGAGAACATCATGGAACAACTCACTGAGTGTAAAGCTTTCAGAAATATATCC 660  
  
QY 661 AGGACAACTGAAGAAAGAAATGTTAGATACAGCAGAAATGCAAGTGCAGACGG 720  
DB 661 AGGACAACTGAAGAAAGAAATGTTAGATACAGCAGAAATGCAAGTGCAGACGG 720  
  
QY 721 CTGTGATGATAGAAATAGGGAACAACTGTTGACCAACAGCTGAGCAACGCGGAAT 780  
DB 721 CTGTGATGATAGAAATAGGGAACAACTGTTGACCAACAGCTGAGCAACGCGGAAT 780  
  
QY 781 TAACTGATGTGGAAGCCCAAGTATTAATCAGACCAAGACTTCACTCAGCTCTTGG 840  
DB 781 TAACTGATGTGGAAGCCCAAGTATTAATCAGACCAAGACTTCACTCAGCTCTTGG 840  
  
QY 841 AACACTCCCTCTCGACAAACAAATTTGGAAGAAACAGATTTTGGACCAACAGTGAATAA 900  
DB 841 AACACTCCCTCTCGACAAACAAATTTGGAAGAAACAGATTTTGGACCAACAGTGAATAA 900

841 AACACTCCCTCTCGACAAACAAATTTGGAAGAAACAGATTTTGGACCAACAGTGAATAA 900  
901 ACAAATTCAGAGATAGAACAGTTTCTAGAAAAGAGGTGCTAGCTATGGAAGACAGC 960  
901 ACAAATTCAGAGATAGAACAGTTTCTAGAAAAGAGGTGCTAGCTATGGAAGACAGC 960  
961 ACATCATCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCA 1020  
961 ACATCATCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCA 1020  
1021 AGCAAAATTCATCATTTGAAGAACTAGAAAAAAAATAGTGAAGTCCACCGTGAATAT 1080  
1021 AGCAAAATTCATCATTTGAAGAACTAGAAAAAAAATAGTGAAGTCCACCGTGAATAT 1080  
1081 CAGTTCTTCAAAAGAGCAACATGATCTCATGAGACAGTTAATACTTACTGACTATGA 1140  
1081 CAGTTCTTCAAAAGAGCAACATGATCTCATGAGACAGTTAATACTTACTGACTATGA 1140  
1141 TGTCCACATCAAACTCAGCTAAGGACCCCACTGTTGCTAAGAGAAACAATCAGCTTCA 1200  
1141 TGTCCACATCAAACTCAGCTAAGGACCCCACTGTTGCTAAGAGAAACAATCAGCTTCA 1200  
1201 GAGACTGTGCTGAAGTATTCAAAATCAGGACACACCAAAATGGCATCTACACGTTAA 1260  
1201 GAGACTGTGCTGAAGTATTCAAAATCAGGACACACCAAAATGGCATCTACACGTTAA 1260  
1261 TCCTTAATTTACAGAAAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGCGCGGT 1320  
1261 TCCTTAATTTACAGAAAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGCGCGGT 1320  
1321 GGAACAATTTACAGCACTGAGGATGGGAGCTGATTTTTCAGAGGACTTGGAAAGAA 1380  
1321 GGAACAATTTACAGCACTGAGGATGGGAGCTGATTTTTCAGAGGACTTGGAAAGAA 1380  
1381 ATAAAGTGGATTTGGTAAACCTTTCAGGAGAAATATTGGCTGGGAAATAGTGTTCGC 1440  
1381 ATAAAGTGGATTTGGTAAACCTTTCAGGAGAAATATTGGCTGGGAAATAGTGTTCGC 1440  
1441 AACTGACTATTCAGCAACGCTATGTGCTTAAATACACCTTAAAGACTGGGAGGAA 1500  
1441 AACTGACTATTCAGCAACGCTATGTGCTTAAATACACCTTAAAGACTGGGAGGAA 1500  
1501 AGGCTTACTATTTGATGAACATTTCTATCTCAAGTGAAGACTCAATTTATAGGATTC 1560  
1501 AGGCTTACTATTTGATGAACATTTCTATCTCAAGTGAAGACTCAATTTATAGGATTC 1560  
1561 ACCTTAAAGGACTTACAGGACACAGCGGCAAAATTAAGCAGCATCAGCCAAACAGG 1620  
1561 ACCTTAAAGGACTTACAGGACACAGCGGCAAAATTAAGCAGCATCAGCCAAACAGG 1620  
1621 ATTTTAGCACAAAGGATGGAGACAAACGAAATGTTTTCGAAATGTTCAAAATGCTAA 1680  
1621 ATTTTAGCACAAAGGATGGAGACAAACGAAATGTTTTCGAAATGTTCAAAATGCTAA 1680  
1681 CAGAGGCTGGTGGTTGATGTCATGTCCTTCCAACTTGAACGGATGACTATCCAC 1740  
1681 CAGAGGCTGGTGGTTGATGTCATGTCCTTCCAACTTGAACGGATGACTATCCAC 1740  
1741 AGAGGCAGAACACAAATAAGTTCAACGGCATTAATGCTACTCTGGAAGGCTCAGGCT 1800  
1741 AGAGGCAGAACACAAATAAGTTCAACGGCATTAATGCTACTCTGGAAGGCTCAGGCT 1800  
1801 ATTTCGCTCAAGGGCCACCAACATGATGATCCGACAGCAGATTTCTAAACATCCAG 1860  
1801 ATTTCGCTCAAGGGCCACCAACATGATGATCCGACAGCAGATTTCTAAACATCCAG 1860  
1861 CCTGAGGAACTGTCTCGAACTATTTTCAAGAGCTTAAGCCAGTGCATGGAAGTCA 1920  
1861 CCTGAGGAACTGTCTCGAACTATTTTCAAGAGCTTAAGCCAGTGCATGGAAGTCA 1920  
1921 CTGGGCACTGTGCTCTTCCACCAAGAGGCGGTGCTCGGTGCTGAGCGGACCCACA 1980  
1921 CTGGGCACTGTGCTCTTCCACCAAGAGGCGGTGCTCGGTGCTGAGCGGACCCACA 1980

QY 1981 TGCTCCAGATTAGAGCCTGTAACCTTTATCACTTAACTTGCATCACTTAAACGGACCAA 2040  
DB |||||  
QY 1981 TGCTCCAGATTAGAGCCTGTAACCTTTATCACTTAACTTGCATCACTTAAACGGACCAA 2040  
DB |||||  
QY 2041 GCAAGACCTTAACATCCATAATTGATGATGACAGAACACCTATGCAAAAGATGAACCG 2100  
DB |||||  
QY 2041 GCAAGACCTTAACATCCATAATTGATGATGACAGAACACCTATGCAAAAGATGAACCG 2100  
DB |||||  
QY 2101 AGGCTGAGAAATCAGACTGACAGTTTACAGACGCTGCTGCACAAACAGAAATGTTATG 2160  
DB |||||  
QY 2101 AGGCTGAGAAATCAGACTGACAGTTTACAGACGCTGCTGCACAAACAGAAATGTTATG 2160  
DB |||||  
QY 2161 CAAAGTTTATCAGTAAATACTGGAACACAGAACACTTATGTTATACAAATACAGATCATCT 2220  
DB |||||  
QY 2161 CAAAGTTTATCAGTAAATACTGGAACACAGAACACTTATGTTATACAAATACAGATCATCT 2220  
DB |||||  
QY 2221 TCGAACTGCATCTTCTGAGCACTGTTTATACATGTTGTAATACCCATATCTCTGAAT 2280  
DB |||||  
QY 2221 TCGAACTGCATCTTCTGAGCACTGTTTATACATGTTGTAATACCCATATCTCTGAAT 2280  
DB |||||  
QY 2281 TC 2282  
DB |||||  
QY 2281 TC 2282

RESULT 4  
AAZ92215  
ID AAZ92215 standard; DNA; 2269 BP.  
AC AAZ92215;  
XX  
XX 19-MAY-2000 (first entry)  
DE Human angiotensin-2 (Ang-2) nucleotide sequence.  
XX  
KW Human; angiotensin-2; Ang-2; aminophospholipid; vascularised tumour;  
KW unconjugated anti-aminophospholipid antibody; tumour blood vessel marker;  
KW cancer; treatment; angiogenesis; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200002584-A2.  
PN  
XX  
PD 20-JAN-2000.  
XX  
PF 12-JUL-1999; 99WO-US015600.  
XX  
PR 13-JUL-1999; 98US-0092672P.  
PR 02-DEC-1998; 98US-0110608P.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA  
XX  
XX Thorne PE, Ran S;  
PI  
XX  
XX WPI; 2000-182175/16.  
DR P-PSDB; AAY78906.  
XX  
PT New composition for killing tumor vascular endothelial cells for treating  
PT solid tumors, comprises unconjugated anti-aminophospholipid antibody.  
XX  
PS Disclosure; Page 222; 226pp; English.  
XX  
CC This sequence represents the human angiotensin-2 (Ang-2) nucleotide  
CC sequence. Ang-2 is a naturally occurring angiogenesis antagonist when  
CC vascular endothelial growth factor (VEGF) levels are low, and generally  
CC counteracts the blood vessel maturation and stability mediated by Ang-1.  
CC Ang-1 is a naturally occurring angiogenesis agonist, and is a maturation  
CC or stabilisation factor, converting immature vessels to mature vessels.  
CC Both Ang-1 and Ang-2 are useful in a therapeutic approach to the  
CC treatment of vascularised tumours. The invention relates to a composition  
CC comprising an anti-aminophospholipid antibody, or its antigen binding  
CC region. The composition is used to kill tumour vasculature endothelial

CC cells. Aminophospholipids are stable and specific markers accessible on  
CC the luminal surface of tumour blood vessels. Ang-1 or Ang-2 may be used  
CC in the composition of the invention. The composition is used to treat  
CC malignant or benign vascularised tumours in animals, especially large  
CC tumours  
XX  
SQ Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;  
Query Match 99.4%; Score 2269; DB 3; Length 2269;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 TGGGTTGGTGTGTTTATCTCTCCAGCCTTGAGGGAGGAAACAACTGTAGGATCTGGGG 67  
DB |||||  
QY 1 TGGGTTGGTGTGTTTATCTCTCCAGCCTTGAGGGAGGAAACAACTGTAGGATCTGGGG 60  
DB |||||  
QY 68 AGAGAGGAACAAAGACCGTGAAAGCTGCTCTGTAAAAGCTGACACAGCCCTCCCAAGTG 127  
DB |||||  
QY 61 AGAGAGGAACAAAGACCGTGAAAGCTGCTCTGTAAAAGCTGACACAGCCCTCCCAAGTG 120  
DB |||||  
QY 128 AGCAGGACTGTTTCTCCCACTGCAATCTGACAGTTTACTTGCAATGCTGAGAGAGACACAG 187  
DB |||||  
QY 121 AGCAGGACTGTTTCTCCCACTGCAATCTGACAGTTTACTTGCAATGCTGAGAGAGACACAG 180  
DB |||||  
QY 188 CAGTAAAAAACAGGTTTGTCTACTGAAAAAGAGAGAAAGAGACTTTTCATTGACGGACC 247  
DB |||||  
QY 181 CAGTAAAAAACAGGTTTGTCTACTGAAAAAGAGAGAAAGAGACTTTTCATTGACGGACC 240  
DB |||||  
QY 248 CAGCCATGGCAGCTGACAGCCCTGCTGTTTACAGCGGACGAGCTCGGAGCTCTGGAGCT 307  
DB |||||  
QY 241 CAGCCATGGCAGCTGACAGCCCTGCTGTTTACAGCGGACGAGCTCGGAGCTCTGGAGCT 300  
DB |||||  
QY 308 GTGTTTGCCTCAAGTTTGTCTAAAGCTGCTGGTTTATTACTGAAGAAAGAACTGTGCAGAT 367  
DB |||||  
QY 301 GTGTTTGCCTCAAGTTTGTCTAAAGCTGCTGGTTTATTACTGAAGAAAGAACTGTGCAGAT 360  
DB |||||  
QY 368 TGTTTTCTTTACTCTGAGCTGTGATCTTGTCTTGCCCGCAGCCTATAACAACTTTCCGAA 427  
DB |||||  
QY 361 TGTTTTCTTTACTCTGAGCTGTGATCTTGTCTTGCCCGCAGCCTATAACAACTTTCCGAA 420  
DB |||||  
QY 428 GAGCATGACAGCATAGGAAAGAGCAATATCAGTCCAGATGGTCTGCGAGCTACAC 487  
DB |||||  
QY 421 GAGCATGACAGCATAGGAAAGAGCAATATCAGTCCAGATGGTCTGCGAGCTACAC 480  
DB |||||  
QY 488 TTTCTCTCTGCGAGATGGCAACTGCGCTCTTCTCCAGCCCTACGTTCCAAATGC 547  
DB |||||  
QY 481 TTTCTCTCTGCGAGATGGCAACTGCGCTCTTCTCCAGCCCTACGTTCCAAATGC 540  
DB |||||  
QY 548 TGTG CAGAGGAGCGCGCTGCAATACGATGACTCGGTG CAGAGGCTGCAAGTGTGGA 607  
DB |||||  
QY 541 TGTG CAGAGGAGCGCGCTGCAATACGATGACTCGGTG CAGAGGCTGCAAGTGTGGA 600  
DB |||||  
QY 608 GAACATCATGGAACAACTCAGTGGCTTAATGAGCTTGAGAAATTTATCCAGACAA 667  
DB |||||  
QY 601 GAACATCATGGAACAACTCAGTGGCTTAATGAGCTTGAGAAATTTATCCAGACAA 660  
DB |||||  
QY 668 CATGAAGAAAGAAATGTTAGATACAGCAGAAATGCAGTACAGAACCCAGCGCTGTGAT 727  
DB |||||  
QY 661 CATGAAGAAAGAAATGTTAGATACAGCAGAAATGCAGTACAGAACCCAGCGCTGTGAT 720  
DB |||||  
QY 728 GATGAATATAGGACAAACCTGTTGAACAAACAGCTGAGCAAAACCGGAGATTAACGGA 787  
DB |||||  
QY 721 GATGAATATAGGACAAACCTGTTGAACAAACAGCTGAGCAAAACCGGAGATTAACGGA 780  
DB |||||  
QY 788 TGTGGAACCCCAAGTATTAATCAGACCCAGCAGCTTGAACCTTCAGCTCTTGGAAACCTC 847  
DB |||||  
QY 781 TGTGGAACCCCAAGTATTAATCAGACCCAGCAGCTTGAACCTTCAGCTCTTGGAAACCTC 840  
DB |||||  
QY 848 CCTCTCGCAACAACTTTGGAAAAACAGATTTTGGAC CAGACCTGAGTGAATTAACAAAT 907  
DB |||||  
QY 841 CCTCTCGCAACAACTTTGGAAAAACAGATTTTGGAC CAGACCTGAGTGAATTAACAAAT 900  
DB |||||  
QY 908 GCAAGATGAACAGCTTTCTTAGAAAAAGAGGCTGTAGCTATGGAAGACAGCATCAT 967

901 GCAGATTAAGACAGTTTCTAGAAAAGAGTGCTAGCTATGGAAGACAGACATCAT 960  
968 CCAACTACAGTCAATAAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAGCAAAA 1027  
961 CCAACTACAGTCAATAAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAGCAAAA 1020  
1028 TTCATCATTAAGAACTAGAAAAAATAATAGTACATGCGACCGTGAATAATTCAGTTCT 1087  
1021 TTCATCATTAAGAACTAGAAAAAATAATAGTACATGCGACCGTGAATAATTCAGTTCT 1080  
1088 TCAAAAGCAGCAGCATGATCTCATGAGAGAGATTAATACTTACTGACTATGATGCCAC 1147  
1081 TCAAAAGCAGCAGCATGATCTCATGAGAGAGATTAATACTTACTGACTATGATGCCAC 1140  
1148 ATCAAACTCAGCTAAGGACCCCACTGTTGTTAAAGAGAGAAACAAATCAGCTTCAGAGACTG 1207  
1141 ATCAAACTCAGCTAAGGACCCCACTGTTGTTAAAGAGAGAAACAAATCAGCTTCAGAGACTG 1200  
1208 TGCTGAAGTATTCAAATCAGGACACACCAAAATGGGATCTACAGCTTAAACATTCCTCTAA 1267  
1201 TGCTGAAGTATTCAAATCAGGACACACCAAAATGGGATCTACAGCTTAAACATTCCTCTAA 1260  
1268 TTCTACAGAGAGATCAAGCCCTACTGCTGACATGGAAGCTGGAGGAGGCGGTGGACAAT 1327  
1261 TTCTACAGAGAGATCAAGCCCTACTGCTGACATGGAAGCTGGAGGAGGCGGTGGACAAT 1320  
1328 TATTCAGCAGCTGAGGATGGCAGCGTTGATTTTCAGAGAGCTTGGAAAGAAATATAAGT 1387  
1321 TATTCAGCAGCTGAGGATGGCAGCGTTGATTTTCAGAGAGCTTGGAAAGAAATATAAGT 1380  
1388 GGGATTTGTPAACCCCTTCAGGAGAAATATTCGGCTGGGAAATGAGTTGTTTCGCAACTGAC 1447  
1381 GGGATTTGTPAACCCCTTCAGGAGAAATATTCGGCTGGGAAATGAGTTGTTTCGCAACTGAC 1440  
1448 TAATCAGCAGCTATGCTTAAATAACCTTAAAGCTGGAGGAGGAAATCAGGCTTA 1507  
1441 TAATCAGCAGCTATGCTTAAATAACCTTAAAGCTGGAGGAGGAAATCAGGCTTA 1500  
1508 CTCAATGTATGAACATTTCTATCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA 1567  
1501 CTCAATGTATGAACATTTCTATCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA 1560  
1568 AGGACTTACAGGAGCAGCGGCAAAATAAGCAGCATCAGCAACACAGGAAATGATTTAG 1627  
1561 AGGACTTACAGGAGCAGCGGCAAAATAAGCAGCATCAGCAACACAGGAAATGATTTAG 1620  
1628 CACAAAGGATGGAGACACGACAAATGTTTGCATATGTTCAAAATGCTTAACAGAGG 1687  
1621 CACAAAGGATGGAGACACGACAAATGTTTGCATATGTTCAAAATGCTTAACAGAGG 1680  
1688 CTGGTGGTTTGTGTCATGCTGCTTCCAACTTGAACGGAATGATCTATCCACAGAGGCA 1747  
1681 CTGGTGGTTTGTGTCATGCTGCTTCCAACTTGAACGGAATGATCTATCCACAGAGGCA 1740  
1748 GAACACAAATAAGTTCAACGGCATTAATGCTACTCTGGAAGGCTCAGGCTATTCGCT 1807  
1741 GAACACAAATAAGTTCAACGGCATTAATGCTACTCTGGAAGGCTCAGGCTATTCGCT 1800  
1808 CAAAGGCCAACCAATGATGATCCGACAGAGATTTCTAAACATCCAGTCCACCTGAGG 1867  
1801 CAAAGGCCAACCAATGATGATCCGACAGAGATTTCTAAACATCCAGTCCACCTGAGG 1860  
1868 AACTGTCTCGAATTTTCAAGACCTTAAGCCAGTGCACTGAAAGCTCAGGCTGGCA 1927  
1861 AACTGTCTCGAATTTTCAAGACCTTAAGCCAGTGCACTGAAAGCTCAGGCTGGCA 1920  
1928 CTGTGCTCTTCCACACAGAGGCGGTGCTGCTGCTGCTGACGGGACCCACATGCTCCA 1987  
1921 CTGTGCTCTTCCACACAGAGGCGGTGCTGCTGCTGCTGACGGGACCCACATGCTCCA 1980  
1988 GATTAGAGCCTGTAAACTTTATCACTTAAACTTCATCACTTAAACCGAACCAAGAC 2047

1981 GATTAGAGCCTGTAAACTTTATCACTTAAACTTCATCACTTAAACCGAACCAAGAC 2040  
2048 CCTAAACATCCATATTTGATTAGACAGACACACCTATGCAAGATGAACCGAGGCTGA 2107  
2041 CCTAAACATCCATATTTGATTAGACAGACACACCTATGCAAGATGAACCGAGGCTGA 2100  
2108 GAATCAGACTGACAGTTTACAGACGCTGCTGTCAACCAAGAAATCTTATGTGCAAGTTT 2167  
2101 GAATCAGACTGACAGTTTACAGACGCTGCTGTCAACCAAGAAATCTTATGTGCAAGTTT 2160  
2168 ATCAGTAAATAAATCGAAAAACAGACACTTATGTTTATACAAATCAGATCATCTTGAAC 2227  
2161 ATCAGTAAATAAATCGAAAAACAGACACTTATGTTTATACAAATCAGATCATCTTGAAC 2220  
2228 GCATTTCTTGAAGACTGTTTATACACTGTGTAAATACCCATATGTCCT 2276  
2221 GCATTTCTTGAAGACTGTTTATACACTGTGTAAATACCCATATGTCCT 2269

RESULT 5  
AAZ92213  
ID AAZ92213 standard; DNA; 2269 BP.  
XX  
AC AAZ92213;  
XX 19-MAY-2000 (first entry)  
DT Human angiotensin-2 nucleotide sequence.  
XX  
DE Angiotensin-2; Ang-2; vascular endothelial growth factor; tumour;  
XX Angiotensin-2; Ang-2; vascular endothelial growth factor; tumour;  
XX vascularisation; angiogenesis; blood vessel maturation; malignant;  
XX benign; binding ligand; cancer; aminophospholipid; ss.  
XX Homo sapiens.  
XX WO200002587-A1.  
XX 20-JAN-2000.  
XX  
XX 12-JUL-1999; 99WO-US015668.  
XX PF  
XX 13-JUL-1998; 98US-0092589P.  
XX PR 02-DEC-1998; 98US-0110600P.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX Thorpe PE, Ran S;  
XX  
XX WPI; 2000-182177/16.  
XX P-PSDB; AAY78903.  
XX  
XX Binding ligand for aminophospholipid used in the treatment of  
XX vascularized tumors, comprises targeting component and therapeutic agent.  
XX  
XX Disclosure; Page 257; 267pp; English.  
XX  
XX This sequence represents the human angiotensin-2 (Ang-2) nucleotide  
XX sequence. Ang-2 is a naturally occurring angiogenesis antagonist when  
XX vascular endothelial growth factor (VEGF) levels are low, and generally  
XX counteracts the blood vessel maturation and stability mediated by Ang-1.  
XX Ang-1 is a naturally occurring angiogenesis agonist, and is a maturation  
XX or stabilisation factor, converting immature vessels to mature vessels.  
XX Both Ang-1 and Ang-2 are useful in a therapeutic approach to the  
XX treatment of vascularised tumours. The invention relates to a binding  
XX ligand comprising a targeting agent that binds to an aminophospholipid,  
XX linked to a therapeutic agent (e.g. Ang-2). Aminophospholipids are stable  
XX vessels. The binding ligand induces coagulation (thrombosis) in tumour  
XX vessels. The binding ligand causes tumour necrosis (possibly by cell- or complement-  
XX mediated cytotoxicity and/or apoptosis). The binding ligands are used to  
XX treat vascularised tumours, malignant or benign, in animals, especially  
XX large tumours

|                            |      |   |      |
|----------------------------|------|---|------|
| SQ                         |      | Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;     |      |
| Query Match                |      | 99.4%; Score 2269; DB 3; Length 2269;                           |      |
| Best Local Similarity      |      | 100.0%; Pred. No. 0;  |      |
| Matches 2269; Conservative |      | 0; Mismatches 0; Indels 0; Gaps 0;                              |      |
| QY                         | 8    | TGGGTTGGTGTATCTCTCCAGCCTTGGAGGGGAAACAACATGTAGGATCTGGGG          | 67   |
| DB                         | 1    | TGGGTTGGTGTATCTCTCCAGCCTTGGAGGGGAAACAACATGTAGGATCTGGGG          | 60   |
| QY                         | 68   | AGAGAGGAACAAGACCGGTGAAGCTGCTGTAAAGCTCACAGCCCTCCCAAGTG           | 127  |
| DB                         | 61   | AGAGAGGAACAAGACCGGTGAAGCTGCTGTAAAGCTCACAGCCCTCCCAAGTG           | 120  |
| QY                         | 128  | AGCAGGACTGTTCTTCCCACTGCAATCTCACAGTTTACTTGCATGCTGGAGAGAACACAG    | 187  |
| DB                         | 121  | AGCAGGACTGTTCTTCCCACTGCAATCTCACAGTTTACTTGCATGCTGGAGAGAACACAG    | 180  |
| QY                         | 188  | CAGTAAAAACCAAGTTTGCTACTGGAAAAAGAGAAAGAGACTTTCATTTGACGGACC       | 247  |
| DB                         | 181  | CAGTAAAAACCAAGTTTGCTACTGGAAAAAGAGAAAGAGAGACTTTCATTTGACGGACC     | 240  |
| QY                         | 248  | CAGCCATGCGAGGTAGCAGCCCTGGGTTTACAGCGGACGAGCTCGGACTCTGGAAGT       | 307  |
| DB                         | 241  | CAGCCATGCGAGGTAGCAGCCCTGGGTTTACAGCGGACGAGCTCGGACTCTGGAAGT       | 300  |
| QY                         | 308  | GTGTTTGCCTCAAGTTTGTAAAGCTGCTGGTTTAACTGAGAAAGAAATGTGCAGAT        | 367  |
| DB                         | 301  | GTGTTTGCCTCAAGTTTGTAAAGCTGCTGGTTTAACTGAGAAAGAAATGTGCAGAT        | 360  |
| QY                         | 368  | TGTTTTCTTTACTCTGAGCTGTGATCTTGCTGTGGCGGAGCTATTAACAATTTTCGGAA     | 427  |
| DB                         | 361  | TGTTTTCTTTACTCTGAGCTGTGATCTTGCTGTGGCGGAGCTATTAACAATTTTCGGAA     | 420  |
| QY                         | 428  | GAGCATGAGACGATAGGAAGAAGCAATATCAGCTCCAGCATGGTCTCGAGCTACAC        | 487  |
| DB                         | 421  | GAGCATGAGACGATAGGAAGAAGCAATATCAGCTCCAGCATGGTCTCGAGCTACAC        | 480  |
| QY                         | 488  | TTTTCTCTCTCCAGAGATGGACAACTGCCGCTCTTCTCCAGCCCTACGTTCCAAATGC      | 547  |
| DB                         | 481  | TTTTCTCTCTCCAGAGATGGACAACTGCCGCTCTTCTCCAGCCCTACGTTCCAAATGC      | 540  |
| QY                         | 548  | TGTGACAGGGGACGGCGGCTCGAATACGATGACTCGGTGCGAGGCTGCAAGTGTGTA       | 607  |
| DB                         | 541  | TGTGACAGGGGACGGCGGCTCGAATACGATGACTCGGTGCGAGGCTGCAAGTGTGTA       | 600  |
| QY                         | 608  | GAACTCATGGAAACAACACTCAGTGGCTATGAAGCTTGAAGATTATATCCAGGACAA       | 667  |
| DB                         | 601  | GAACTCATGGAAACAACACTCAGTGGCTATGAAGCTTGAAGATTATATCCAGGACAA       | 660  |
| QY                         | 668  | CATGAAGAAAGAAATGGTAGAGATACAGCAAGTGCAGTACAGAACCCAGCGGCTGTGAT     | 727  |
| DB                         | 661  | CATGAAGAAAGAAATGGTAGAGATACAGCAAGTGCAGTACAGAACCCAGCGGCTGTGAT     | 720  |
| QY                         | 728  | GATAGAAATAGGGACAAACCTGTTGAAACAAACAGCTGAGGAAACCGGGAAGTTAACTGA    | 787  |
| DB                         | 721  | GATAGAAATAGGGACAAACCTGTTGAAACAAACAGCTGAGGAAACCGGGAAGTTAACTGA    | 780  |
| QY                         | 788  | TGTGGAAGCCCAAGTATTAAATCAGACCAACGAGACTTGAACCTTCAGCTCTTGGAACTTC   | 847  |
| DB                         | 781  | TGTGGAAGCCCAAGTATTAAATCAGACCAACGAGACTTGAACCTTCAGCTCTTGGAACTTC   | 840  |
| QY                         | 848  | CCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCAAGCAGCTGAAATTAACAAATTT  | 907  |
| DB                         | 841  | CCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCAAGCAGCTGAAATTAACAAATTT  | 900  |
| QY                         | 908  | GCAAGATAGAACAGTTTCTTGAAGAAAGAGGTGCTAGCTATGGAAGACAGCAATCAT       | 967  |
| DB                         | 901  | GCAAGATAGAACAGTTTCTTGAAGAAAGAGGTGCTATGGAAGACAGCAATCAT           | 960  |
| QY                         | 968  | CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTTACAGGTTAGTATCAACGACAAA       | 1027 |
| DB                         | 961  | CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTTACAGGTTAGTATCAACGACAAA       | 1020 |
| QY                         | 1028 | TTCCATCATTTGAAGAACTAGAAAAAATAAGTACTGCTCCACGGTGAATAATTCAGTTCT    | 1087 |
| DB                         | 1021 | TTCCATCATTTGAAGAACTAGAAAAAATAAGTACTGCTCCACGGTGAATAATTCAGTTCT    | 1080 |
| QY                         | 1088 | TCAAAAGCAGCAACATGATCTCATGGAGACAGTGTAACTTACTGATGATGTCAC          | 1147 |
| DB                         | 1081 | TCAAAAGCAGCAACATGATCTCATGGAGACAGTGTAACTTACTGATGATGTCAC          | 1140 |
| QY                         | 1148 | ATCAAACTCAGTAAAGGACCCACCTGTTCTTAAAGAAACAAATCAGCTTCAGAGACTG      | 1207 |
| DB                         | 1141 | ATCAAACTCAGTAAAGGACCCACCTGTTCTTAAAGAAACAAATCAGCTTCAGAGACTG      | 1200 |
| QY                         | 1208 | TGCTGAAGTATTCAAAATCAGGACACACCAAAATGGCATCTACAGTTTAACTTCCCTAA     | 1267 |
| DB                         | 1201 | TGCTGAAGTATTCAAAATCAGGACACACCAAAATGGCATCTACAGTTTAACTTCCCTAA     | 1260 |
| QY                         | 1268 | TTCTACAGAGAGATCAAGGGCTACTGTGACATGGAAGCTGGAGGGGGTGGACAAAT        | 1327 |
| DB                         | 1261 | TTCTACAGAGAGATCAAGGGCTACTGTGACATGGAAGCTGGAGGGGGTGGACAAAT        | 1320 |
| QY                         | 1328 | TATTACAGCGAGTGAAGGATGCGAGGTTGATTTTCAGAGGACTTGGAAAGAAATATAAGT    | 1387 |
| DB                         | 1321 | TATTACAGCGAGTGAAGGATGCGAGGTTGATTTTCAGAGGACTTGGAAAGAAATATAAGT    | 1380 |
| QY                         | 1388 | GGGATTTGGTAAACCTTTCAGGAGAAATATTGGCTGGGAAATGAGTTTGTTCGCAACTGAC   | 1447 |
| DB                         | 1381 | GGGATTTGGTAAACCTTTCAGGAGAAATATTGGCTGGGAAATGAGTTTGTTCGCAACTGAC   | 1440 |
| QY                         | 1448 | TAAATCAGCAACGCTATGCTTAAATACACCTTAAAGACTGGGAAAGGAAATGAGGCTTA     | 1507 |
| DB                         | 1441 | TAAATCAGCAACGCTATGCTTAAATACACCTTAAAGACTGGGAAAGGAAATGAGGCTTA     | 1500 |
| QY                         | 1508 | CTCATTTGATGAACATTTCTCTCAAGTGAAGAACTCAATATTAGATTTCACCTTAA        | 1567 |
| DB                         | 1501 | CTCATTTGATGAACATTTCTCTCAAGTGAAGAACTCAATATTAGATTTCACCTTAA        | 1560 |
| QY                         | 1568 | AGGACTTACAGGACAGCGCGGCAAAATTAAGCAGCATCAGCCAAACCCAGGAAATGATTTAG  | 1627 |
| DB                         | 1561 | AGGACTTACAGGACAGCGCGGCAAAATTAAGCAGCATCAGCCAAACCCAGGAAATGATTTAG  | 1620 |
| QY                         | 1628 | CACAAAGATGGAGACACGACAAATGTTTGCNAATGTTTCACAAATGTTCAACAGGAGG      | 1687 |
| DB                         | 1621 | CACAAAGATGGAGACACGACAAATGTTTGCNAATGTTTCACAAATGTTCAACAGGAGG      | 1680 |
| QY                         | 1688 | CTGGTGGTTTCAATGCTGCTTCCAACTTGAACGAAATGTACTATCCACAGAGGCA         | 1747 |
| DB                         | 1681 | CTGGTGGTTTCAATGCTGCTTCCAACTTGAACGAAATGTACTATCCACAGAGGCA         | 1740 |
| QY                         | 1748 | GAACAAATTAAGTTTCAACCGCATTTAAATGGTACTTCTGGAAGAGGCTCAGGCTATTCGCT  | 1807 |
| DB                         | 1741 | GAACAAATTAAGTTTCAACCGCATTTAAATGGTACTTCTGGAAGAGGCTCAGGCTATTCGCT  | 1800 |
| QY                         | 1808 | CAAGGCCCAACCATGATGATCCGACGACGAGATTTCTTAAACATCCAGTCCACCTGAGG     | 1867 |
| DB                         | 1801 | CAAGGCCCAACCATGATGATCCGACGACGAGATTTCTTAAACATCCAGTCCACCTGAGG     | 1860 |
| QY                         | 1868 | AATGCTCTCGAACTTATTTTCAAGAGCTTAAAGCCAGTGCACCTGAAAGTCAAGGCTGCGCA  | 1927 |
| DB                         | 1861 | AATGCTCTCGAACTTATTTTCAAGAGCTTAAAGCCAGTGCACCTGAAAGTCAAGGCTGCGCA  | 1920 |
| QY                         | 1928 | CTGTGCTCTTTCACCAACAGAGGGCGTGTGCTGGTGTCTGACGGGACCCACATGCTCA      | 1987 |
| DB                         | 1921 | CTGTGCTCTTTCACCAACAGAGGGCGTGTGCTGGTGTCTGACGGGACCCACATGCTCA      | 1980 |
| QY                         | 1988 | GATTAGAGCCTGTAACTTTTACTTAACTTGAACATCTTAACTTAACTTAACTTAACTTAACTT | 2047 |
| DB                         | 1981 | GATTAGAGCCTGTAACTTTTACTTAACTTGAACATCTTAACTTAACTTAACTTAACTTAACTT | 2040 |
| QY                         | 2048 | CCTTAAACATCCATATTTGATTAGACAGAACACCTTATGCAAGATGAACCCGAGGCTGA     | 2107 |
| DB                         | 2041 | CCTTAAACATCCATATTTGATTAGACAGAACACCTTATGCAAGATGAACCCGAGGCTGA     | 2100 |





QY 1208 TGTCTGAAGTATTTCAAAATCAGGACACACCAAAATGGCATCTACAGTTAACTTCCCTAA 1267  
Db 1201 TGTCTGAAGTATTTCAAAATCAGGACACACCAAAATGGCATCTACAGTTAACTTCCCTAA 1260  
QY 1268 TTCTACAGAAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAGAGCGGGGTGACAAAT 1327  
Db 1261 TTCTACAGAAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAGAGCGGGGTGACAAAT 1320  
QY 1328 TATTACAGCCACTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGATATAAAGT 1387  
Db 1321 TATTACAGCCACTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGATATAAAGT 1380  
QY 1388 GGGATTGTGTAACCCCTTCAGGAGAAATATTTGGCTGGGAATGAGTTTGTTCGCCAACTGCAC 1447  
Db 1381 GGGATTGTGTAACCCCTTCAGGAGAAATATTTGGCTGGGAATGAGTTTGTTCGCCAACTGCAC 1440  
QY 1448 TAAATCAGCAACCGCTATGCTTAAATAACACCTTAAAGACTGGGAAGGGAATGAGGCTTA 1507  
Db 1441 TAAATCAGCAACCGCTATGCTTAAATAACACCTTAAAGACTGGGAAGGGAATGAGGCTTA 1500  
QY 1508 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTATAGGATTCACCTTAA 1567  
Db 1501 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTATAGGATTCACCTTAA 1560  
QY 1568 AGGACTTACAGGACAGCCCGCAAAATTAAGCAGCATCAGCCAAACAGGAAATGATTTTAG 1627  
Db 1561 AGGACTTACAGGACAGCCCGCAAAATTAAGCAGCATCAGCCAAACAGGAAATGATTTTAG 1620  
QY 1628 CACAAAGGATGAGACAAACGAAATGATTTTGCAAAATGTTTCAAAATGCTTAAACGGAG 1687  
Db 1621 CACAAAGGATGAGACAAACGAAATGATTTTGCAAAATGTTTCAAAATGCTTAAACGGAG 1680  
QY 1688 CTGGTGTGTTGATGATGTTGCTTCCAACTTGACGGAATGTAATCCACAGAGCA 1747  
Db 1681 CTGGTGTGTTGATGATGTTGCTTCCAACTTGACGGAATGTAATCCACAGAGCA 1740  
QY 1748 GAACCAAAATAGTTTCAACGGCAATTAATGGTACTACTGGAAGGCTCAGGCTATTGCT 1807  
Db 1741 GAACCAAAATAGTTTCAACGGCAATTAATGGTACTACTGGAAGGCTCAGGCTATTGCT 1800  
QY 1808 CAAGGCCAACATGATGATCGGACGACGATTTCTAAACATCCAGTCCACCTGAGG 1867  
Db 1801 CAAGGCCAACATGATGATCGGACGACGATTTCTAAACATCCAGTCCACCTGAGG 1860  
QY 1868 AACTGTCTCGAACTATTTTCAAGACTTAAGCCGAGTGCACGTGAAGTCAAGGCTGCGCA 1927  
Db 1861 AACTGTCTCGAACTATTTTCAAGACTTAAGCCGAGTGCACGTGAAGTCAAGGCTGCGCA 1920  
QY 1928 CTGTGTCTCTTCCACACAGAGGGGCTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1987  
Db 1921 CTGTGTCTCTTCCACACAGAGGGGCTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1980  
QY 1988 GATTAGAGCTGTAACTTTATCACTTAACTTGATCACTTAAAGGACCAAGCAAGAC 2047  
Db 1981 GATTAGAGCTGTAACTTTATCACTTAACTTGATCACTTAAAGGACCAAGCAAGAC 2040  
QY 2048 CCTAAACATCCATAATTTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA 2107  
Db 2041 CCTAAACATCCATAATTTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA 2100  
QY 2108 GAATCAGACTGACAGTTTACAGACGCTGCTGTCAACACCAAGAAATGTTATGTCAGTTT 2167  
Db 2101 GAATCAGACTGACAGTTTACAGACGCTGCTGTCAACACCAAGAAATGTTATGTCAGTTT 2160  
QY 2168 ATCAGTAAATAATCGGAAAACAGAACATTAATGTTTATACAAATACAGATCATCTTGAAC 2227  
Db 2161 ATCAGTAAATAATCGGAAAACAGAACATTAATGTTTATACAAATACAGATCATCTTGAAC 2220  
QY 2228 GCAATCTTCTGAGCACTGTTTATACACTGTGTAATAATACCCATATGTCCT 2276  
Db 2221 GCAATCTTCTGAGCACTGTTTATACACTGTGTAATAATACCCATATGTCCT 2269

RESULT 7  
AAS70958  
ID AAS70958 standard; cDNA; 2269 BP.  
XX AAS70958;  
XX 13-FEB-2002 (first entry)  
XX DNA encoding novel human diagnostic protein #6762.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US008631.  
XX 31-MAR-2000; 2000US-00540217.  
XX 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
XX P-PSDB; ABG06771.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX Claim 1; SEQ ID NO 6762; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;  
Query Match 99.4%; Score 2269; DB 5; Length 2269;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 TGGGTGGTGGTTATCTCTCCAGCCCTTGAGGGAGGAAACAACACTGTAGGATCTGGGG 67  
Db 1 TGGGTGGTGGTTATCTCTCCAGCCCTTGAGGGAGGAAACAACACTGTAGGATCTGGGG 60  
QY 68 AGAGAGGAAACAAGACCGCTGAAAGCTCTCTGTAAGAGCTGACACAGCCCTCCCAAGTG 127

Db 61 AGAGAGAAACAAAGGACCGTGAAGCTGCTCTCTAAAGCTGACACAGCCCTCCCAAGTG 120  
Qy 128 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGCTGAGAGAAACACAG 187  
Db 121 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGCTGAGAGAAACACAG 180  
Qy 188 CAGTAAACACAGGTTTGTCTGGAAGAAAGAGAGAAAGAGACATTTCAATTGACCGACC 247  
Db 181 CAGTAAACACAGGTTTGTCTGGAAGAAAGAGAGAAAGAGACATTTCAATTGACCGACC 240  
Qy 248 CAGCCATGCGAGCTAGCAGCCCTGGTCTTTCAGACGCGACAGCTCGGAGCTCTGACAGT 307  
Db 241 CAGCCATGCGAGCTAGCAGCCCTGGTCTTTCAGACGCGACAGCTCGGAGCTCTGACAGT 300  
Qy 308 GTCTTTGCCCTCAAGTTTGTCTAGCTGCTGCTGTTTAACTTGAAGAAAGAAATGTGGCAGAT 367  
Db 301 GTCTTTGCCCTCAAGTTTGTCTAGCTGCTGCTGTTTAACTTGAAGAAAGAAATGTGGCAGAT 360  
Qy 368 TGTCTTTCTTTTACTCTGAGCTGTGATCTTGTCTTGGCGGCGAGCTTAAACAACTTTGGAA 427  
Db 361 TGTCTTTCTTTTACTCTGAGCTGTGATCTTGTCTTGGCGGCGAGCTTAAACAACTTTGGAA 420  
Qy 428 GAGCATGCGACGATAGGAAGAGCAATATCAGGTCACGATGGGTCTTGCAGCTACAC 487  
Db 421 GAGCATGCGACGATAGGAAGAGCAATATCAGGTCACGATGGGTCTTGCAGCTACAC 480  
Qy 488 TTTTCTCTCTGCGAGATGACAACTGCGCGCTCTTCTCCAGCGCCCTTACGTGCTCAATGC 547  
Db 481 TTTTCTCTCTGCGAGATGACAACTGCGCGCTCTTCTCCAGCGCCCTTACGTGCTCAATGC 540  
Qy 548 TGTGCGAGGAGCGCGCGCTCGAATAACGATGATCTGGTGCAGAGGCTGCAAGTGTGGA 607  
Db 541 TGTGCGAGGAGCGCGCGCTCGAATAACGATGATCTGGTGCAGAGGCTGCAAGTGTGGA 600  
Qy 608 GAACATCATGGAACAAACACTCAGTGGCTTAAAGAGCTTGAATTTATATCCAGGACAA 667  
Db 601 GAACATCATGGAACAAACACTCAGTGGCTTAAAGAGCTTGAATTTATATCCAGGACAA 660  
Qy 668 CATGAAGAAAGAAATGGTAGATACAGCAGAAATGACAGTACAGAACCCAGACGGCTGTGAT 727  
Db 661 CATGAAGAAAGAAATGGTAGATACAGCAGAAATGACAGTACAGAACCCAGACGGCTGTGAT 720  
Qy 728 GATAGAAATAGGACAAACCTGTTGAAACCAACAGCTTGAGCAAACCGCGGAAGTTAACTGA 787  
Db 721 GATAGAAATAGGACAAACCTGTTGAAACCAACAGCTTGAGCAAACCGCGGAAGTTAACTGA 780  
Qy 788 TGTGGAAGCCCAAGTATTAATCAGACCAAGAGCTTGAACCTCAGCTCTTGGAACTC 847  
Db 781 TGTGGAAGCCCAAGTATTAATCAGACCAAGAGCTTGAACCTCAGCTCTTGGAACTC 840  
Qy 848 CCTCTCGACAAACAAATTTGGAAGAAACAGATTTTGGACGAGACCAAGTGAATTAACAAATTT 907  
Db 841 CCTCTCGACAAACAAATTTGGAAGAAACAGATTTTGGACGAGACCAAGTGAATTAACAAATTT 900  
Qy 908 GCAAGATAGGAACAGTTTCTTAGAAAAAGAGGCTAGCTATGGAAGACCAAGCAGCATCAT 967  
Db 901 GCAAGATAGGAACAGTTTCTTAGAAAAAGAGGCTAGCTATGGAAGACCAAGCAGCATCAT 960  
Qy 968 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTTGTAGTATCCAGGCAAAA 1027  
Db 961 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTTGTAGTATCCAGGCAAAA 1020  
Qy 1028 TTCCATCATTTGAAGAACTTAGAAAAAAATAGTCACTGCGACGCTGGAATTAATTCAGTTCT 1087  
Db 1021 TTCCATCATTTGAAGAACTTAGAAAAAAATAGTCACTGCGACGCTGGAATTAATTCAGTTCT 1080  
Qy 1088 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTTAACTTACTGACTATGATGTCCAC 1147  
Db 1081 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTTAACTTACTGACTATGATGTCCAC 1140  
Qy 1148 ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAGAGAAACAAATCAGCTTCAGAGACTG 1207  
Db 1141 ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAGAGAAACAAATCAGCTTCAGAGACTG 1200

Qy 1208 TGCTGAAGTATTTCAAAATCAGGACACACCAAAATGSCATCTACACGTTTAAACATTTCCCTAA 1267  
Db 1201 TGCTGAAGTATTTCAAAATCAGGACACACCAAAATGSCATCTACACGTTTAAACATTTCCCTAA 1260  
Qy 1268 TTCTACAGAAAGAGATCAAGGCGCTACTGTGACATGGAAGCTGGAAGGAGGGGGTGGCAAT 1327  
Db 1261 TTCTACAGAAAGAGATCAAGGCGCTACTGTGACATGGAAGCTGGAAGGAGGGGGTGGCAAT 1320  
Qy 1328 TATTCAGCCAGCTGAGGATGCGAGCGTTGATTTTTCAGAGGACTGGAAGAAATATATAAGT 1387  
Db 1321 TATTCAGCCAGCTGAGGATGCGAGCGTTGATTTTTCAGAGGACTGGAAGAAATATATAAGT 1380  
Qy 1388 GGGATTTGTTAAACCTTTTCAGGAGAAATTTGGCTGGGAAATGATTTGTTTTCGCAACTGAC 1447  
Db 1381 GGGATTTGTTAAACCTTTTCAGGAGAAATTTGGCTGGGAAATGATTTGTTTTCGCAACTGAC 1440  
Qy 1448 TAAATCAGCAACGCTATGTGCTTAAAAATACACCTTTAAAGACTGGGAAGGGAATGAGGCTTA 1507  
Db 1441 TAAATCAGCAACGCTATGTGCTTAAAAATACACCTTTAAAGACTGGGAAGGGAATGAGGCTTA 1500  
Qy 1508 CTCATTGTATGAACATTTCTACTCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA 1567  
Db 1501 CTCATTGTATGAACATTTCTACTCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA 1560  
Qy 1568 AGGACTTACAGGACAGCGCGGCAAAATAGCAGCATCAGCCAAACCCAGGAAATGATTTAG 1627  
Db 1561 AGGACTTACAGGACAGCGCGGCAAAATAGCAGCATCAGCCAAACCCAGGAAATGATTTAG 1620  
Qy 1628 CACAAAGGATGGAAGACAAACGACAAATGTATTTTCAAAATGTTTCAAAATGCTTAAACAGGAG 1687  
Db 1621 CACAAAGGATGGAAGACAAACGACAAATGTATTTTCAAAATGTTTCAAAATGCTTAAACAGGAG 1680  
Qy 1688 CTGCTGCTTGTGATGATGTGCTCTTCCAACTTTGAAACCGGAATGTACTATCCACAGAGGCA 1747  
Db 1681 CTGCTGCTTGTGATGATGTGCTCTTCCAACTTTGAAACCGGAATGTACTATCCACAGAGGCA 1740  
Qy 1748 GAACAAATTAAGTTCAAACGGCAATTAATGGTACTACTGGAAGGCTCAGGCTATTCGCT 1807  
Db 1741 GAACAAATTAAGTTCAAACGGCAATTAATGGTACTACTGGAAGGCTCAGGCTATTCGCT 1800  
Qy 1808 CRAAGGCCAACCACTGATGATCGACAGCAGATTTCTAAACATCCAGTCCACCTCAGG 1867  
Db 1801 CRAAGGCCAACCACTGATGATCGACAGCAGATTTCTAAACATCCAGTCCACCTCAGG 1860  
Qy 1868 AACTGTCTCGAACTATTTTCAAAGACTTAAAGCCAGTGCACTGAAAGTCAACGCTCGGCA 1927  
Db 1861 AACTGTCTCGAACTATTTTCAAAGACTTAAAGCCAGTGCACTGAAAGTCAACGCTCGGCA 1920  
Qy 1928 CTGTGCTCTTCCACACAGAGGGGCTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1987  
Db 1921 CTGTGCTCTTCCACACAGAGGGGCTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1980  
Qy 1988 GATTAGAGCTGTAAACTTTTATCACTTAACTTTGCACTTAAACGAGCAACCAAGCAAGAC 2047  
Db 1981 GATTAGAGCTGTAAACTTTTATCACTTAACTTTGCACTTAAACGAGCAACCAAGCAAGAC 2040  
Qy 2048 CCTAAACATCCATAATTTGTGATTTAGACAGAACACCTATGCAAGATGAAACCCGAGGCTGA 2107  
Db 2041 CCTAAACATCCATAATTTGTGATTTAGACAGAACACCTATGCAAGATGAAACCCGAGGCTGA 2100  
Qy 2108 GAATCAGACTGACAGTTTACAGCGCTGTGTCACAAACCAAGAAATGTTATGTGCAAGTTT 2167  
Db 2101 GAATCAGACTGACAGTTTACAGCGCTGTGTCACAAACCAAGAAATGTTATGTGCAAGTTT 2160  
Qy 2168 ATCAGTAAATTAACCTGGAAGAACAGAACTTATGTTATACAAATCAGATCATCTTGGAACT 2227  
Db 2161 ATCAGTAAATTAACCTGGAAGAACAGAACTTATGTTATACAAATCAGATCATCTTGGAACT 2220  
Qy 2228 GCATTTCTTCTGAGCACTGTTTATACACTGTGTAATATACCCATATGCTCT 2276  
Db 2221 GCATTTCTTCTGAGCACTGTTTATACACTGTGTAATATACCCATATGCTCT 2269

|                            |   |
|----------------------------|---|
| RESULT 8                   |   |
| ABZ35349                   |   |
| ID                         | ABZ35349 standard; cDNA; 2269 BP.   |
| XX                         | AC ABZ35349;  |
| XX                         | DT 05-FEB-2003 (first entry)  |
| XX                         | DE Human gene expression profile polynucleotide SEQ ID NO 460.  |
| XX                         | KW Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery; bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast; tumour; microarray; genome mapping; antibiotic; antiviral; antifungal; gene expression; gene; ss.   |
| XX                         | OS Homo sapiens.  |
| XX                         | PN WO200274979-A2.  |
| XX                         | XX 26-SEP-2002.   |
| XX                         | PD 20-MAR-2002; 2002WO-US008456.  |
| XX                         | PF 20-MAR-2001; 2001US-0276947P.  |
| XX                         | PR (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  |
| XX                         | PA Wan J, Wang Y;   |
| XX                         | PI WPI; 2002-740862/80.   |
| XX                         | DR New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer.  |
| XX                         | PS Example 3; Page 609-610; 850pp; English.   |
| XX                         | CC The invention relates to a gene expression profile comprising one or more genes (ABZ34899-ABZ35692) and generated from a cell type. The cell type is a coronary artery endothelium, umbilical artery or vein endothelium, aortic endothelium, dermal microvascular endothelium, pulmonary artery endothelium, myometrium microvascular endothelium, keratinocyte epithelium, bronchial epithelium, mammary epithelium, prostate epithelium, renal cortical epithelium, renal proximal tubule epithelium, small airway epithelium, renal epithelium, umbilical artery smooth muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle, dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes, aortic smooth muscle, mesangial cells, coronary artery smooth muscle, bronchial smooth muscle, uterine smooth muscle, lung fibroblast, osteoblasts or prostate stromal cell. The gene expression profile is used for determining the level of RNA expression for a sample, determining the phenotype of a cell and distinguishing cell types. The gene or a protein expression profile is useful in identifying disease pathologies involving alterations of gene expression. The assessment of expression profiles may provide meaningful information with respect to tumour type and stage, treatment methods, and prognosis. The gene or protein expression profile may also be used for creating microarrays. The microarray is useful for genetic and physical mapping of genomes, DNA sequencing, genetic or medical diagnosis, genotyping of organisms, confirming cell or tissue identifications and in identifying promising antibiotics, antiviral or antifungal agents |
| XX                         | SQ Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;  |
| Query Match                | 99.4%; Score 2269; DB 6; Length 2269;   |
| Best Local Similarity      | 100.0%; Pred. No. 0;  |
| Matches 2269; Conservative | 0; Mismatches 0; Indels 0; Gaps 0;  |
| Qy                         | 8 TGGGTTGGTGTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGATCTGGGG 67   |
| Db                         | 1 TGGGTTGGTGTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGATCTGGGG 60   |
| Qy                         | 68 AGAGAGGAACAAGACCGTGAAGAGCTGCTGTGTAAAAAGCTGACACAGCCCTCCCAAGTG 127   |
| Db                         | 61 AGAGAGGAACAAGACCGTGAAGAGCTGCTGTGTAAAAAGCTGACACAGCCCTCCCAAGTG 120   |
| Qy                         | 128 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTATGCTGGAGAGAACACAG 187  |
| Db                         | 121 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTATGCTGGAGAGAACACAG 180  |
| Qy                         | 188 CAGTAAAAACCAAGGTTTCTACTGAAAAAGAGGAAGAGAGCTTTTCATTGACGGACC 247   |
| Db                         | 181 CAGTAAAAACCAAGGTTTCTACTGAAAAAGAGGAAGAGAGCTTTTCATTGACGGACC 240   |
| Qy                         | 248 CAGCCATGCGCAGCTAGCAGCCCTCGGTTTCAGACGGCAGCAGCTCGGAGCTCTGAGAGT 307  |
| Db                         | 241 CAGCCATGCGCAGCTAGCAGCCCTCGGTTTCAGACGGCAGCAGCTCGGAGCTCTGAGAGT 300  |
| Qy                         | 308 GTGTTTGGCCTCAAGTTTGTAAAGTGTCTGTTTATTACTGAAGAAAGATGTGGCAGAT 367  |
| Db                         | 301 GTGTTTGGCCTCAAGTTTGTAAAGTGTCTGTTTATTACTGAAGAAAGATGTGGCAGAT 360  |
| Qy                         | 368 TGTGTTTCTTACTCTGAGCTGTGATCTTGTGTCGCGCAGCCTATAACAACCTTTCCGGA 427   |
| Db                         | 361 TGTGTTTCTTACTCTGAGCTGTGATCTTGTGTCGCGCAGCCTATAACAACCTTTCCGGA 420   |
| Qy                         | 428 GAGCATGGACAGCATAGGAAGAAGCAATATACAGTCCAGCATGGGTCTTCGAGCTACAC 487   |
| Db                         | 421 GAGCATGGACAGCATAGGAAGAAGCAATATACAGTCCAGCATGGGTCTTCGAGCTACAC 480   |
| Qy                         | 488 TTTCTCTCTCCAGAGATGGACAACCTGCGGCTCTTCTCCAGCCCTTACGTTGTCCTCAATGC 547  |
| Db                         | 481 TTTCTCTCTCCAGAGATGGACAACCTGCGGCTCTTCTCCAGCCCTTACGTTGTCCTCAATGC 540  |
| Qy                         | 548 TGTGAGAGGAGCGCGCTCGAATACGATGACCTCGGTGCGAGAGGCTGCAAGTGTCTGA 607  |
| Db                         | 541 TGTGAGAGGAGCGCGCTCGAATACGATGACCTCGGTGCGAGAGGCTGCAAGTGTCTGA 600  |
| Qy                         | 608 GAACATCATGGAACAAACACTCAGTGTGCTAATGAAGCTTGAGAAATTATATCCAGGACAA 667   |
| Db                         | 601 GAACATCATGGAACAAACACTCAGTGTGCTAATGAAGCTTGAGAAATTATATCCAGGACAA 660   |
| Qy                         | 668 CATGGAAGAAGAAATGGTAGATACAGACAGAAATGCAGTACAGACACAGAGCGGTGTGAT 727  |
| Db                         | 661 CATGGAAGAAGAAATGGTAGATACAGACAGAAATGCAGTACAGACACAGAGCGGTGTGAT 720  |
| Qy                         | 728 GATAGAAATAGGGAACAAACCTGTTGAACCAACAGCTCAGCAACAGCCGGAAGTTAACTGA 787   |
| Db                         | 721 GATAGAAATAGGGAACAAACCTGTTGAACCAACAGCTCAGCAACAGCCGGAAGTTAACTGA 780   |
| Qy                         | 788 TGTGGAAGCCCAAGTATTAAATCAGACCAAGAGACTTGAACCTTCAGCTCTTGGAAACATC 847   |
| Db                         | 781 TGTGGAAGCCCAAGTATTAAATCAGACCAAGAGACTTGAACCTTCAGCTCTTGGAAACATC 840   |
| Qy                         | 848 CCTCTCGAACAACAAATTTGGAACACAGATTTTGGACCAGACCCAGTGAATAAACAATTT 907  |
| Db                         | 841 CCTCTCGAACAACAAATTTGGAACACAGATTTTGGACCAGACCCAGTGAATAAACAATTT 900  |
| Qy                         | 908 GCAAGATAAGAACAGTTTCTTAGAAAAAGAGGTGTAGCTATGGAAGCAAGACATCAT 967   |
| Db                         | 901 GCAAGATAAGAACAGTTTCTTAGAAAAAGAGGTGTAGCTATGGAAGCAAGACATCAT 960   |
| Qy                         | 968 CCACTACAGTCAATAAAGAGAGAGAGATCAGCTACAGGTGTTAGTATTCAGCAACAAA 1027   |
| Db                         | 961 CCACTACAGTCAATAAAGAGAGAGAGATCAGCTACAGGTGTTAGTATTCAGCAACAAA 1020   |
| Qy                         | 1028 TTCCATCATTCGAAGCTAGAAAAAATAATAGTACTGCCAGCGGTGAATAATTCAGTTCT 1087   |
| Db                         | 1021 TTCCATCATTCGAAGCTAGAAAAAATAATAGTACTGCCAGCGGTGAATAATTCAGTTCT 1080   |
| Qy                         | 1088 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTTAATAACTTACTGACTATGATGTCAC 1147  |
| Db                         | 1081 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTTAATAACTTACTGACTATGATGTCAC 1140  |
| Qy                         | 1148 ATCAAACTCAGCTAAGGACCCCACTGTTTGCTTAAAGAGAACAAATCAGCTTCAGAGACTG 1207   |

Db 1141 ATCAAACTCAGCTAAGGACCCCACTGTTGCTAAAGAAAGCAAAATCAGCTTCAGAGACTG 1200  
Qy 1208 TGCTGAAGTATTCAAAATCAGGACACACCAAAATGCGATCTACACGTTTAACTTCCCTTAA 1267  
Db 1201 TGCTGAAGTATTCAAAATCAGGACACACCAAAATGCGATCTACACGTTTAACTTCCCTTAA 1260  
Qy 1268 TTCTACAGAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAAGGCGGGTGGCAAT 1327  
Db 1261 TTCTACAGAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAAGGCGGGTGGCAAT 1320  
Qy 1328 TATTACGACGATGAGATGCGAGCGCTGATTTTTCAGAGGACTTGGAAGATATATAAAGT 1387  
Db 1321 TATTACGACGATGAGATGCGAGCGCTGATTTTTCAGAGGACTTGGAAGATATATAAAGT 1380  
Qy 1388 GGAATTTGGTAACCCCTTCAGGAAATATTTGGCTGGGAAATGAGTTTGTTCGCAACTGAC 1447  
Db 1381 GGAATTTGGTAACCCCTTCAGGAAATATTTGGCTGGGAAATGAGTTTGTTCGCAACTGAC 1440  
Qy 1448 TAATCAGCAACGCTATGTGCTTAAATAACACCTTAAAGACTGGGAAGGAAATGAGGCTTA 1507  
Db 1441 TAATCAGCAACGCTATGTGCTTAAATAACACCTTAAAGACTGGGAAGGAAATGAGGCTTA 1500  
Qy 1508 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA 1567  
Db 1501 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA 1560  
Qy 1568 AGACTTCAGGACGACGCGGCAAAATATAGCAGCATCAGCAACAGGAAATGATTTTAG 1627  
Db 1561 AGACTTCAGGACGACGCGGCAAAATATAGCAGCATCAGCAACAGGAAATGATTTTAG 1620  
Qy 1628 CACAAAGGATGGAGACAAACACAAATGTTTTCAAATGTTTCAAAATGCTTAAACAGGAG 1687  
Db 1621 CACAAAGGATGGAGACAAACACAAATGTTTTCAAATGTTTCAAAATGCTTAAACAGGAG 1680  
Qy 1688 CTGGTGGTTGATGATGCTGCTTCCAACTTGAACGGAATGTACTATCCACAGAGGCA 1747  
Db 1681 CTGGTGGTTGATGATGCTGCTTCCAACTTGAACGGAATGTACTATCCACAGAGGCA 1740  
Qy 1748 GAACAAATAAGCTTCAACGGCATTAATGCTACTGTAAGGCTCAGGCTATTCGCT 1807  
Db 1741 GAACAAATAAGCTTCAACGGCATTAATGCTACTGTAAGGCTCAGGCTATTCGCT 1800  
Qy 1808 CAAGGACCAACCATGATGATCGACACGAGATTTTCTAAACATCCAGTCCACCTGAGG 1867  
Db 1801 CAAGGACCAACCATGATGATCGACACGAGATTTTCTAAACATCCAGTCCACCTGAGG 1860  
Qy 1868 AACTGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCACCTGAAAGTCAAGGCTGCGCA 1927  
Db 1861 AACTGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCACCTGAAAGTCAAGGCTGCGCA 1920  
Qy 1928 CTGTGCTCTTCCACACAGAGGGGCTGCTCGGTGCTGACGGGACCCACATGCTCCA 1987  
Db 1921 CTGTGCTCTTCCACACAGAGGGGCTGCTCGGTGCTGACGGGACCCACATGCTCCA 1980  
Qy 1988 GATTAGAGCTGTAAACCTTTATCACTTAAACCTTGCATCACTTAACGGAACCAAGCAAGAC 2047  
Db 1981 GATTAGAGCTGTAAACCTTTATCACTTAAACCTTGCATCACTTAACGGAACCAAGCAAGAC 2040  
Qy 2048 CCTAAACATCCATAATTTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA 2107  
Db 2041 CCTAAACATCCATAATTTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA 2100  
Qy 2108 GAATCAGACTGACGATTTACAGAGCGTGTGTCAACACCAAGATGTTATGTGCAAGTTT 2167  
Db 2101 GAATCAGACTGACGATTTACAGAGCGTGTGTCAACACCAAGATGTTATGTGCAAGTTT 2160  
Qy 2168 ATCAGTAAATACTGGAAGAAACAGAACTTATGTTATACAAATACAGATCATCTTTGGAAC 2227  
Db 2161 ATCAGTAAATACTGGAAGAAACAGAACTTATGTTATACAAATACAGATCATCTTTGGAAC 2220  
Qy 2228 GCATTCTTCTGAGCACTGTTTATACACTGTGTTAAATACCCATATGTCCT 2276  
|||||

Db 2221 GCATTCTTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCCT 2269

## RESULT 9

ABK47716

ID ABK47716 standard; DNA; -2269 BP.

XX

AC ABK47716;

XX

DT 02-JUL-2002 (first entry)

XX

DE DNA encoding human angiopoietin-2.

XX

Human; immunoconjugate; anti-vascular endothelial growth factor antibody;  
anti-VEGF antibody; monoclonal antibody 2C3 ATCC PTA 1595; VEGF receptor;  
VEGFR2; KDR/Flk-1; VEGFR1; Flt-1; angiogenesis; macular degeneration;  
ocular neovascular disease; cancer; vascularised solid tumour; AIDS;  
metastatic tumour; endothelial cell proliferation; inflammatory disorder;  
atherosclerosis; diabetic retinopathy; corneal graft rejection;  
acquired immune deficiency syndrome; infection; restenosis; fungal ulcer;  
sickle cell anaemia; endometriosis; angiopoietin-2; gene; ds.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FH 350..1840

FT /\*tag= a

FT /product= "Angiopoietin-2"

XX

PN AU200179401-A.

XX

PD 06-DEC-2001.

XX

PF 12-OCT-2001; 2001AU-00079401.

XX

PR 28-APR-2000; 2000AU-00048049.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX

PI Thorpe PE, Brekken RA;

XX

WPI; 2002-281368/33.

DR P-PSDB; AAU77944.

XX

Immuconjugate compositions for treating cancer by inhibiting  
angiogenesis and for delivering a diagnostic agent to tumor, comprises  
anti-vascular endothelial growth factor antibody attached to a biological  
agent.

Disclosure; Page 4 (Sequence listing); 299pp; English.

The present invention relates to antibody-based compositions comprising  
an immunoconjugate such as anti-vascular endothelial growth factor (VEGF)  
antibody (Ab) (or its antigen-binding fragment), attached to a biological  
agent, where the Ab binds to the same epitope as the monoclonal antibody  
(Mab) 2C3 ATCC PTA 1595, and significantly inhibits VEGF binding to the  
VEGF receptor (KDR/Flk-1) without inhibiting VEGF binding to the  
VEGF receptor VEGFR1 (Flt-1). The compositions of the invention are  
useful in therapy, and diagnosis, for inhibiting angiogenesis in an  
animal having ocular neovascular disease or macular degeneration, and for  
delivering a biological agent to a vascularised tumour. The compositions  
can also be used for treating cancer and subjects at risk of developing,  
a vascularised solid tumour, a metastatic tumour or metastases from a  
primary tumour. The composition is useful for specifically inhibiting  
VEGF-induced endothelial cell proliferation, without significantly  
inhibiting VEGF-induced macrophage, osteoclast or chondroblast function.  
The compositions can be used for treating various diseases such as  
inflammatory disorders, atherosclerosis, diabetic retinopathy,  
restenosis, acquired immune deficiency syndrome (AIDS), blood borne  
tumours, corneal graft rejection, Crohn's disease, fungal ulcers,  
infections, sickle cell anaemia, and endometriosis. The present sequence  
encodes human angiopoietin-2. Angiopoietin-2 may be attached or  
functionally associated with anti-VEGF antibodies



|    |  |  |
|----|--|--|
| XX | Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;  |  |
| SQ | Query Match 99.4%; Score 2269; DB 6; Length 2269;<br>Best Local Similarity 100.0%; Pred. No. 0;<br>Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |  |
| QY | 8 TGGGTGGTGTATCTCTCCAGCCTTTGAGGGAGGAAACAACACTGTAGGATCTGGGG 67  | 961 CCAACTACAGTCAATAAAGAGAGAGAAAGATCAGCTACAGGTGTAGTATCAAGCAAAA 1020        |
| DB | 1 TGGGTGGTGTATCTCTCCAGCCTTTGAGGGAGGAAACAACACTGTAGGATCTGGGG 60  | 1028 TTCCATCATTTGAAGAACTAGAAAAAATAAGTACTGCCACGGTGAAATAATTCAGTTCT 1087      |
| QY | 68 AGAGAGAAACAAGACCGTGAAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG 127   | 1021 TTCCATCATTTGAAGAACTAGAAAAAATAAGTACTGCCACGGTGAAATAATTCAGTTCT 1080      |
| DB | 61 AGAGAGAAACAAGACCGTGAAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG 120   | 1088 TCAAAAGCAGCAACATGATCTCATGAGACAGTTAATAACTTACCTGACTATGATGTCAC 1147      |
| QY | 128 ACAGAGACTGTTCTCCCACTGCAATCTGACAGTTTACTGCAATGCTGAGAGAGAACACAG 187   | 1081 TCAAAAGCAGCAACATGATCTCATGAGACAGTTAATAACTTACCTGACTATGATGTCAC 1140      |
| DB | 121 ACAGAGACTGTTCTCCCACTGCAATCTGACAGTTTACTGCAATGCTGAGAGAGAACACAG 180   | 1148 ATCAAACTCAGCTAGGACCCCACTGTTCTTAAAGAGAAACAANTCAGCTTCAGAGACTG 1207      |
| QY | 188 CAGTAAAAACCAAGTTTGTCTACTGGAAAAAGAGGAAAGAGACTTTTCATTGACGGACC 247  | 1141 ATCAAACTCAGCTAGGACCCCACTGTTCTTAAAGAGAAACAANTCAGCTTCAGAGACTG 1200      |
| DB | 181 CAGTAAAAACCAAGTTTGTCTACTGGAAAAAGAGGAAAGAGACTTTTCATTGACGGACC 240  | 1208 TGCTGAAGTATTCAAACTCAGGACACACCAAAATGGCATCTACAGCTTAAACATTCCTTAA 1267    |
| QY | 248 CAGCCATGCGCAGCTAGCAGCCCTGGGTTTCAGACGGCAGAGCTCGGACTCTCGACGT 307   | 1201 TGCTGAAGTATTCAAACTCAGGACACACCAAAATGGCATCTACAGCTTAACTTCCTTAA 1260      |
| DB | 241 CAGCCATGCGCAGCTAGCAGCCCTGGGTTTCAGACGGCAGAGCTCGGACTCTCGACGT 300   | 1268 TTCTACAGAAGAGATCAAGGGCTACTGTGACATGAGAACTGGAGAGGGGGTGACAAAT 1327       |
| QY | 308 GTGTTTGGCCCTCAAGTTTGTCTTAAGCTGCTGGTTTATTACTGAAGAAAGAATGTGCAGAT 367   | 1261 TTCTACAGAAGAGATCAAGGGCTACTGTGACATGAGAACTGGAGAGGGGGTGACAAAT 1320       |
| DB | 301 GTGTTTGGCCCTCAAGTTTGTCTTAAGCTGCTGGTTTATTACTGAAGAAAGAATGTGCAGAT 360   | 1328 TATTCAGCAGCGTGAGGATGGCAGGTTGATTTTCAGAGGACTTCGGAAGATATATAAGT 1387      |
| QY | 368 TGTGTTTCTTACTCTCAGCTGTGATCTTGTCTTGGCCGAGCTATAACAACTTTTCGGAA 427  | 1321 TATTCAGCAGCGTGAGGATGGCAGGTTGATTTTCAGAGGACTTCGGAAGATATATAAGT 1380      |
| DB | 361 TGTGTTTCTTACTCTCAGCTGTGATCTTGTCTTGGCCGAGCTATAACAACTTTTCGGAA 420  | 1388 GGGATTTGTAACCTTCAGGAGAAATATGGCTGGAAATGAGTTTTCGCAACTGAC 1447           |
| QY | 428 GAGCATGGAACGATAGGAAAGAACATATCAGGTTCAGCATGGGTCTCGACTACAC 487  | 1381 GGGATTTGTAACCTTCAGGAGAAATATGGCTGGAAATGAGTTTTCGCAACTGAC 1440           |
| DB | 421 GAGCATGGAACGATAGGAAAGAACATATCAGGTTCAGCATGGGTCTCGACTACAC 480  | 1448 TAATCAGCAACGCTATGCTTTAAATAACA CTTTAAAGACTGGGAAGGAAATGAGGCTTA 1507     |
| QY | 488 TTTCTCTCTGCAGAGATGGAACAACCTGCGCTCTTCTCCAGCCCTAGCTGCTCAATGC 547   | 1441 TAATCAGCAACGCTATGCTTTAAATAACA CTTTAAAGACTGGGAAGGAAATGAGGCTTA 1500     |
| DB | 481 TTTCTCTCTGCAGAGATGGAACAACCTGCGCTCTTCTCCAGCCCTAGCTGCTCAATGC 540   | 1508 CTGATGTTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTTAGATTCACCTTAA 1567       |
| QY | 548 TGTGAGAGGAGCGGCCCTCGAATACGATGACTCGGTGACAGAGCTGCAAGTCTGGA 607   | 1501 CTGATGTTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTTAGATTCACCTTAA 1560       |
| DB | 541 TGTGAGAGGAGCGGCCCTCGAATACGATGACTCGGTGACAGAGCTGCAAGTCTGGA 600   | 1568 AGGACTTACAGGAGCAGCGCCCAAAATAAGCAGCATCAGCCAAACAGGAAATGATTTTAG 1627     |
| QY | 608 GAAATCATGGAAGAAACAACACTCAGTGGCTATGAGCTTGAATTTATATTCAGGACAA 667   | 1561 AGGACTTACAGGAGCAGCGCCCAAAATAAGCAGCATCAGCCAAACAGGAAATGATTTTAG 1620     |
| DB | 601 GAAATCATGGAAGAAACAACACTCAGTGGCTAATGAGCTTGAATTTATATTCAGGACAA 660  | 1628 CAAAAAGATGGAGAACACGACAAATGATTTGCAAAATGTTTCACAAATGCTTAAACAGGAG 1687    |
| QY | 668 CATGAAGAAAGAAATGGTAGATACAGCAGAAATGCAGTACAGAACCCAGCGCTGTGAT 727   | 1621 CAAAAAGATGGAGAACACGACAAATGATTTGCAAAATGTTTCACAAATGCTTAAACAGGAG 1680    |
| DB | 661 CATGAAGAAAGAAATGGTAGATACAGCAGAAATGCAGTACAGAACCCAGCGCTGTGAT 720   | 1688 CTGGTGTGTTGATGCTGCTTCCAACTTGGAACGGAATGTACTATCCACAGAGCA 1747           |
| QY | 728 GATAGAAATAGGAGCAAAACCTTTGAAACCAACAGCTGAGCAAAACCGGAAAGTTAACTGA 787  | 1681 CTGGTGTGTTGATGCTGCTTCCAACTTGGAACGGAATGTACTATCCACAGAGCA 1740           |
| DB | 721 GATAGAAATAGGAGCAAAACCTTTGAAACCAACAGCTGAGCAAAACCGGAAAGTTAACTGA 780  | 1748 GAAACAAATTAAGTTTCAACGGCATTTAAATGGTACTTACTTGGAAAGGCTCAGGCTATTCGCT 1807 |
| QY | 788 TGTGAGCCCAAGTATTAAATCAGACACAGACTTGAACCTTCAGCTCTTGGAAACATCTC 847  | 1741 GAAACAAATTAAGTTTCAACGGCATTTAAATGGTACTTACTTGGAAAGGCTCAGGCTATTCGCT 1800 |
| DB | 781 TGTGAAAGCCCAAGTATTAAATCAGACCAACGAGACTTGAACTTTCAGCTCTTGGAAACATCTC 840   | 1808 CAAGGCCAACCAATGATGATCCGACACGAGATTTTCTAAACATCCCATCCCTGACCTGAGG 1867    |
| QY | 848 CCTCTCGAACAACAAATGGAAAAACAGATTTTGGACCAAGCCAGTGAATAAACAATTT 907   | 1801 CAAGGCCAACCAATGATGATCCGACACGAGATTTTCTAAACATCCCATCCCTGACCTGAGG 1860    |
| DB | 841 CCTCTCGAACAACAAATGGAAAAACAGATTTTGGACCAAGCCAGTGAATAAACAATTT 900   | 1868 AACTGTCTCGAACTATTTTCAAGACTTTAAAGCTTAAAGCTGCACTGAAAGTCAAGGCTGCGCA 1927 |
| QY | 908 GCAAGATAAGAACAGTTTCTAGAAAAAGAGGTGCTAGCTATGGAAGACAGCAATCAT 967  | 1861 AACTGTCTCGAACTATTTTCAAGACTTTAAAGCTGCACTGAAAGTCAAGGCTGCGCA 1920        |
| DB | 901 GCAAGATAAGAACAGTTTCTAGAAAAAGAGGTGCTAGCTATGGAAGACAGCAATCAT 960  | 1928 CTGTGCTCTTCCACCAAGAGGGCGGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1987         |
| QY | 968 CCAACTACGTCAATAAAGAGAGAGATCAGCTACAGGTGTAGTATCCAAAGCAAAA 1027   | 1921 CTGTGCTCTTCCACCAAGAGGGCGGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1980         |
| DB |  | 1988 GATTAGAGCCTGTAACTTTTACTTAAACTTGCATCACTTAAACGGACCCAAAGCAAGAC 2047      |
| QY |  | 1981 GATTAGAGCCTGTAACTTTTACTTAAACTTGCATCACTTAAACGGACCCAAAGCAAGAC 2040      |
| DB |  | 2048 CCTAAACATCCATTAATTTGATTTAGACAGAACACCTATGCAAGATGAACCGGCTGCA 2107       |
| QY |  | 2041 CCTAAACATCCATTAATTTGATTTAGACAGAACACCTATGCAAGATGAACCGGCTGCA 2100       |



QY 2108 GAATCAGACTGACAGTTTACAGACGCTGTGTCTCAACCAAGAAATGTTATGTCAAGTTT 2167  
DB 2101 GAATCAGACTGACAGTTTACAGACGCTGTGTCTCAACCAAGAAATGTTATGTCAAGTTT 2160  
QY 2168 ATCAGTAATAACTGGAACACAGACACTTATGTTATACATACAGATCATCTTGGAACT 2227  
DB 2161 ATCAGTAATAACTGGAACACAGACACTTATGTTATACATACAGATCATCTTGGAACT 2220  
QY 2228 GCATTTCTTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCCT 2276  
DB 2221 GCATTTCTTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCCT 2269

## RESULT 10

ID ABX12556  
ABX12556 standard; cDNA; 2269 BP.

AC ABX12556;

DT 10-MAY-2003 (first entry)

DE cDNA encoding human angiotensin 2 (Ang-2).

KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;  
KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;  
KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;  
KW cell migration disorder; cell proliferation disorder; neovascularisation;  
KW ischaemia; infarction; tissue graft; transplant;  
KW tie receptor tyrosine kinase; angiotensin 2; ang-2; human; gene; ss.

OS Homo sapiens.

PH Key Location/Qualifiers  
FT CDS 350..1840  
FT /\*tag= a  
FT /product= "Ang-2"  
FT /note= "Angiotensin 2"

PN W02003004529-A2.

XX 16-JAN-2003.

XX 02-JUL-2002; 2002WO-18002524.

XX 02-JUL-2001; 2001US-0302960P.

XX (LICN ) LICENTIA LTD.

XX Alitalo K, Kubo H;

XX WPI; 2003-210341/20.

XX P-PSDB; ABU07855.

XX Identifying modulators of binding between a Tie receptor tyrosine kinase  
XX and an Ephrin ligand, useful for promoting neovascularization, comprises  
XX contacting a Tie receptor with an Ephrin in the presence of a putative  
XX modulator.

XX Disclosure; Page 183-186; 199pp; English.

XX The invention describes a method of identifying a modulator of binding  
XX between a Tie receptor tyrosine kinase and an Ephrin ligand. The method  
XX comprises contacting a Tie receptor composition with an Ephrin  
XX composition in the presence and in the absence of a putative modulator  
XX compound, and detecting the binding between Tie receptor and the Ephrin  
XX in the presence and in the absence of the putative modulator. The method  
XX is useful for identifying a modulator of binding between a Tie receptor  
XX tyrosine kinase and an Ephrin ligand. Modulators identified from the  
XX method are useful in modulating angiogenic processes, including  
XX lymphangiogenesis, for treating diseases associated with aberrant Ephrin-  
XX Tie biology, aberrant growth, migration or proliferation of cells that  
XX express a Tie receptor, or for promoting growth of vessel or

CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or  
CC chronic compound, or a tissue graft or transplant). This sequence encodes  
CC human angiotensin 2 (ang-2), a Tie-2 tyrosine receptor kinase ligand  
XX  
SQ Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;

Query Match 99.4%; Score 2269; DB 8; Length 2269;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGTTGGTGTGTTTATCTCTCCAGCCTTGGAGGGAGGGAACACACTGTAGGATCTGGGG 67

DB 1 TGGTTGGTGTGTTTATCTCTCCAGCCTTGGAGGGAGGGAACACACTGTAGGATCTGGGG 60

QY 68 AGAGAGGAACAAAGGACCGTGAAAGCTGCTCTGTAAAAGCTGACAGACCCCTCCAAAGTG 127

DB 61 AGAGAGGAACAAAGGACCGTGAAAGCTGCTCTGTAAAAGCTGACAGACCCCTCCAAAGTG 120

QY 128 AGCAGGACTGTCTTCCCACTGCAATCTGACAGTTTACTGTCATGCTGGAGAGAACACAG 187

DB 121 AGCAGGACTGTCTTCCCACTGCAATCTGACAGTTTACTGTCATGCTGGAGAGAACACAG 180

QY 188 CAGTAAAAACCAAGCTTGTCTTGGAAAAAGAGAGAAAGAGAACTTTTCAATTGACGACCC 247

DB 181 CAGTAAAAACCAAGCTTGTCTTGGAAAAAGAGAGAAAGAGAACTTTTCAATTGACGACCC 240

QY 248 CAGCCATGCGCAGCTGAGCAGCCCTGCGTTTTCAGACGCGCAGCAGCTCGGAGCTTGGAGCT 307

DB 241 CAGCCATGCGCAGCTGAGCAGCCCTGCGTTTTCAGACGCGCAGCAGCTCGGAGCTTGGAGCT 300

QY 308 GTGTTTGGCCCTCAAGTTTGTCTAAGCTGCTGGTTTATTACTGAAGAAGAAATGTGGCAGAT 367

DB 301 GTGTTTGGCCCTCAAGTTTGTCTAAGCTGCTGGTTTATTACTGAAGAAGAAATGTGGCAGAT 360

QY 368 TGTGTTCTTTTACTCTGAGCTGTGATCTTGTCTTGGCGCAGCTTATAAACAACTTTTCGGAA 427

DB 361 TGTGTTCTTTTACTCTGAGCTGTGATCTTGTCTTGGCGCAGCTTATAAACAACTTTTCGGAA 420

QY 428 GAGCATGGACAGCATAGGAAGCAATATCAGGTTCCAGCTGGGTCCTGCGAGCTACAC 487

DB 421 GAGCATGGACAGCATAGGAAGCAATATCAGGTTCCAGCTGGGTCCTGCGAGCTACAC 480

QY 488 TTTCTCTCTGCGCAGAGATGGACAACTGCGCTCTTCTCCAGCCCTTACGTGTCATGTC 547

DB 481 TTTCTCTCTGCGCAGAGATGGACAACTGCGCTCTTCTCCAGCCCTTACGTGTCATGTC 540

QY 548 TGTGCGAGGGGACGCGCGCTCGAATACGATGACTGGTTCAGAGGCTGCAAGTGTCTGGA 607

DB 541 TGTGCGAGGGGACGCGCGCTCGAATACGATGACTGGTTCAGAGGCTGCAAGTGTCTGGA 600

QY 608 GAACATCATGGAACAAACAACTCAGTGGCTTAATGAAGCTTTGAGAAATTTATATCCAGGACAA 667

DB 601 GAACATCATGGAACAAACAACTCAGTGGCTTAATGAAGCTTTGAGAAATTTATATCCAGGACAA 660

QY 668 CATGAGAAAGAAATGTTAGAGATACAGCAGATGCGAGTACAGNACCAGAGCGGTGTGAT 727

DB 661 CATGAGAAAGAAATGTTAGAGATACAGCAGATGCGAGTACAGNACCAGAGCGGTGTGAT 720

QY 728 GATAGAAATAGGACAAACCTGTTGAACCAACAGCTGAGCAACCGGGAAGTTAACTGA 787

DB 721 GATAGAAATAGGACAAACCTGTTGAACCAACAGCTGAGCAACCGGGAAGTTAACTGA 780

QY 788 TGTGGAAGCCCAAGTATTAATTAATCAGACCCAGACTTTGAACTTTCAGCTTCTTGGAACTC 847

DB 781 TGTGGAAGCCCAAGTATTAATTAATCAGACCCAGACTTTGAACTTTCAGCTTCTTGGAACTC 840

QY 848 CCTCTCGACAAACAAATTTGAAACACAGATTTTGGACCCAGACCCAGTGAATAAACAAATTT 907

DB 841 CCTCTCGACAAACAAATTTGAAACACAGATTTTGGACCCAGACCCAGTGAATAAACAAATTT 900

QY 908 GCAAGATAAGAACAGTTTCTTAGAAGAGAGGCTGTAGCTATGTGAGACAGGACATCAT 967

DB 901 GCAAGATAAGAACAGTTTCTTAGAAGAGAGGCTGTAGCTATGTGAGACAGGACATCAT 960

QY 968 CCACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAGCAAAA 1027  
Db |||||  
QY 961 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAGCAAAA 1020  
Db |||||  
QY 1028 TTCCATCATTTGAAGAACTAGAAAAAATAATAGTAGTGCACGGTGAATAATTCAGTTCT 1087  
Db |||||  
QY 1021 TTCCATCATTTGAAGAACTAGAAAAAATAATAGTAGTGCACGGTGAATAATTCAGTTCT 1080  
Db |||||  
QY 1088 TCAAAAGCAGCAACATGATCTCATGAGACAGTTAATAACTTTACTGACTATCATGTGCCAC 1147  
Db |||||  
QY 1081 TCAAAAGCAGCAACATGATCTCATGAGACAGTTAATAACTTTACTGACTATCATGTGCCAC 1140  
Db |||||  
QY 1148 ATCAAACCTCAGCTAAGGACCCCACTGTTCTTAAAGAAAGCAAAATCAGCTTCAGAGACTG 1207  
Db |||||  
QY 1141 ATCAAACCTCAGCTAAGGACCCCACTGTTCTTAAAGAAAGCAAAATCAGCTTCAGAGACTG 1200  
Db |||||  
QY 1208 TGCTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTACAGTTTAACTTCCTTAA 1267  
Db |||||  
QY 1201 TGCTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTACAGTTTAACTTCCTTAA 1260  
Db |||||  
QY 1268 TTCTCAGAAAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGAGGGGGTGGACAAT 1327  
Db |||||  
QY 1261 TTCTCAGAAAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGAGGGGGTGGACAAT 1320  
Db |||||  
QY 1328 TATTCAGCGACGTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGAAATAAAGT 1387  
Db |||||  
QY 1321 TATTCAGCGACGTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGAAATAAAGT 1380  
Db |||||  
QY 1388 GGGATTTGGTAACTTCAGGAGAAATATGGCTGGGAATGATTTGTTCCCACTGAC 1447  
Db |||||  
QY 1381 GGGATTTGGTAACTTCAGGAGAAATATGGCTGGGAATGATTTGTTCCCACTGAC 1440  
Db |||||  
QY 1448 TAATCAGCAACGCTATGCTTTAAATAACA CTTAAAGACTGGGAAGGAATGAGGCTTA 1507  
Db |||||  
QY 1441 TAATCAGCAACGCTATGCTTTAAATAACA CTTAAAGACTGGGAAGGAATGAGGCTTA 1500  
Db |||||  
QY 1508 CTCAATGTTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1567  
Db |||||  
QY 1501 CTCAATGTTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1560  
Db |||||  
QY 1568 AGGACTTACAGGACAGCCGGCAAAATAGCAGCATCAGCCAAACAGGAAATGATTTAG 1627  
Db |||||  
QY 1561 AGGACTTACAGGACAGCCGGCAAAATAGCAGCATCAGCCAAACAGGAAATGATTTAG 1620  
Db |||||  
QY 1628 CACAAAGGATGAGACACAGCAAAATGATTTGCAAACTGTTCAAAATGCTAACAGGAGG 1687  
Db |||||  
QY 1621 CACAAAGGATGAGACACAGCAAAATGATTTGCAAACTGTTCAAAATGCTAACAGGAGG 1680  
Db |||||  
QY 1688 CTGGTGGTTGATGATGTTGCTTCCAACTTGAAACGGAATGTATATCCACAGAGCA 1747  
Db |||||  
QY 1681 CTGGTGGTTGATGATGTTGCTTCCAACTTGAAACGGAATGTATATCCACAGAGCA 1740  
Db |||||  
QY 1748 GAAACAAATAGTTCAACGGCATTAATATGTTACTTCTGGAAGGCTCAGGCTATTCGCT 1807  
Db |||||  
QY 1741 GAAACAAATAGTTCAACGGCATTAATATGTTACTTCTGGAAGGCTCAGGCTATTCGCT 1800  
Db |||||  
QY 1808 CAAGGCCAACCATGATCATCCGACAGCAGATTTCTAAACATCCAGTCCACCTGAGG 1867  
Db |||||  
QY 1801 CAAGGCCAACCATGATCATCCGACAGCAGATTTCTAAACATCCAGTCCACCTGAGG 1860  
Db |||||  
QY 1868 AACTGTCTCGAACTATTTTCAAAGACTTAAGCCAGTGCACCTGAAAGTCAAGGCTGCGCA 1927  
Db |||||  
QY 1861 AACTGTCTCGAACTATTTTCAAAGACTTAAGCCAGTGCACCTGAAAGTCAAGGCTGCGCA 1920  
Db |||||  
QY 1928 CTGTGCTCTTCCACACAGAGGGGCTGTGCTCGGTGCTGACGGACCCACATGCTCCA 1987  
Db |||||  
QY 1921 CTGTGCTCTTCCACACAGAGGGGCTGTGCTCGGTGCTGACGGACCCACATGCTCCA 1980  
Db |||||  
QY 1988 GATTAGAGCTGTAAACTTTATCACTTAAACTTTGATCACTTAAAGGACCAAGCAAGAC 2047  
Db |||||  
QY 1981 GATTAGAGCTGTAAACTTTATCACTTAAACTTTGATCACTTAAAGGACCAAGCAAGAC 2040  
Db |||||

QY 2048 CCTAAACATCCATAATTTGTGATTAGACAGACACCTATGCAAGATGAACCCGAGCTGA 2107  
Db |||||  
QY 2041 CCTAAACATCCATAATTTGTGATTAGACAGACACCTATGCAAGATGAACCCGAGCTGA 2100  
Db |||||  
QY 2108 GAATCAGACTCAGACTTTTACAGACGCTGTGTCAACCAAGAAATGTTATGTGCAAGTTT 2167  
Db |||||  
QY 2101 GAATCAGACTCAGACTTTTACAGACGCTGTGTCAACCAAGAAATGTTATGTGCAAGTTT 2160  
Db |||||  
QY 2168 ATCAGTAATAACTCGAAAAACAGAAACACTTATGTTTATACAATACAGATCATCTTGAAC 2227  
Db |||||  
QY 2161 ATCAGTAATAACTCGAAAAACAGAAACACTTATGTTTATACAATACAGATCATCTTGAAC 2220  
Db |||||  
QY 2228 GCATTTCTTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCCT 2276  
Db |||||  
QY 2221 GCATTTCTTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCCT 2269  
Db |||||  
RESULT 11  
ADN95380  
ID ADN95380 standard; DNA; 2269 BP.  
XX  
AC ADN95380;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Human BEC/LEC-related gene sequence SeqID303.  
XX  
DE growth; differentiation; blood endothelial cell; BEC;  
KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;  
KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;  
KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;  
KW inflammatory disease; cancer metastasis; lymphatic system; gene; ds;  
KW human.  
XX  
OS Homo sapiens.  
XX  
XX WO2003080640-A1.  
PN  
XX 02-OCT-2003.  
PD  
XX 07-MAR-2003; 2003WO-US006900.  
PF  
XX 07-MAR-2002; 2002US-0363019P.  
PR  
XX (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
PA  
XX Aitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;  
PI  
XX WPI; 2003-876999/81.  
DR P-PSDB; ADN95379.  
DR  
XX  
PS Example 1; SEQ ID NO 303; 176pp; English.  
XX  
CC This invention relates to a method of differentially modulating the  
CC growth or differentiation of blood endothelial cells (BEC) or lymphatic  
CC endothelial cells (LEC) comprises contacting endothelial cells with a  
CC composition comprising an agent that differentially modulates blood or  
CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises  
CC identifying a human subject with lymphoedema and with a mutation in at  
CC least one allele of a gene encoding a LEC protein, where the mutation  
CC correlates with lymphoedema in human subjects, and with the proviso that  
CC the LEC protein is not VEGFR-3; and administering to the subject a  
CC composition comprising a lymphatic growth agent selected from VEGF-C or  
CC VEGF-D polypeptides and polynucleotides. The invention may be useful for  
CC the development of compounds with an antiangiogenic, cytostatic,  
CC vasotropic or antiinflammatory activity or for gene therapy. The method  
CC is useful in modulating the growth or differentiation of blood  
CC endothelial cells or lymphatic endothelial cells, in treating hereditary  
CC lymphoedema, in screening for an endothelial cell disorder or  
CC predisposition to the disorder or in monitoring the efficacy or toxicity  
CC of a drug on endothelial cells. The agent is useful in manufacturing a  
CC medicament for the differential modulation of blood vessel endothelial

CC cell or lymphatic vessel endothelial cell growth or differentiation. The  
CC lymphatic growth agent may also be used in manufacturing a medicament for  
CC the treatment of hereditary lymphoedema resulting from a mutation in a  
CC LEC gene or of other diseases involving the lymphatic vessels, such as  
CC various inflammatory diseases and cancer metastasis via the lymphatic  
CC system. The present sequence is that of a human LEC/BEC differentially  
CC expressed gene which is related to the method of the invention. Note: This  
CC sequence does not appear in the specification but was obtained by the  
CC indexer using the source data given in table 14 of the specification.  
XX  
SQ Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;

|                       |     |   |               |           |              |
|-----------------------|-----|---|---------------|-----------|--------------|
| Query Match           |     | 99.4%;  | Score 2269;   | DB 11;    | Length 2269; |
| Best Local Similarity |     | 100.0%;   | Pred. No. 0;  |           |              |
| Matches 2269;         |     | Conservative 0;   | Mismatches 0; | Indels 0; | Gaps 0;      |
| QY                    | 8   | TGGTGGTCTTTATCTCTCCAGCCTTCAGGAGGAGGAAACAACACTGTAGGATCTGGGG  | 67            |           |              |
| DB                    | 1   | TGGTGGTCTTTATCTCTCCAGCCTTCAGGAGGAGGAAACAACACTGTAGGATCTGGGG  | 60            |           |              |
| QY                    | 68  | AGAGAGGAAACAAAGGACCGTGAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG | 127           |           |              |
| DB                    | 61  | AGAGAGGAAACAAAGGACCGTGAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG | 120           |           |              |
| QY                    | 128 | AGAGAGACTGTTCTCCACTGCAATCTGACAGTTTACTTCATGCTCGGAGAGAACACAG  | 187           |           |              |
| DB                    | 121 | AGCAGGACTGTTCTCCACTGCAATCTGACAGTTTACTTCATGCTCGGAGAGAACACAG  | 180           |           |              |
| QY                    | 188 | CAGTAAACACAGTTTGTCTGAAAGAGGAAAGAGAAAGAGAACTTTTCAATGACGGACC  | 247           |           |              |
| DB                    | 181 | CAGTAAACACAGTTTGTCTGAAAGAGGAAAGAGAAAGAGAACTTTTCAATGACGGACC  | 240           |           |              |
| QY                    | 248 | CAGCCATGGCAGGTAGCAGCCCTGCGTTTTCAGACGACAGCTCGGAGCTCTGACGCT   | 307           |           |              |
| DB                    | 241 | CAGCCATGGCAGGTAGCAGCCCTGCGTTTTCAGACGACAGCTCGGAGCTCTGACGCT   | 300           |           |              |
| QY                    | 308 | GTGTTTCCCTCAAGTTTGTAGCTGCTGCTGTTTATTTACTGAGAAAGATGTGGCAGAT  | 367           |           |              |
| DB                    | 301 | GTGTTTCCCTCAAGTTTGTAGCTGCTGCTGTTTATTTACTGAGAAAGATGTGGCAGAT  | 360           |           |              |
| QY                    | 368 | TGTTTTCTTTACTGAGCTGTGATCTTGTCTGGCCGACGCTTATAACAACTTTTCGAA   | 427           |           |              |
| DB                    | 361 | TGTTTTCTTTACTGAGCTGTGATCTTGTCTGGCCGACGCTTATAACAACTTTTCGAA   | 420           |           |              |
| QY                    | 428 | GAGCATGGACGATAGGAAAGCAATATCAGTCCAGCATGGGTCTCGACGTACAC       | 487           |           |              |
| DB                    | 421 | GAGCATGGACGATAGGAAAGCAATATCAGTCCAGCATGGGTCTCGACGTACAC       | 480           |           |              |
| QY                    | 488 | TTTCTCTCTCCAGAGATGACAACTGCGCTCTTCTCCAGGCCCTTACGTGCCAATGC    | 547           |           |              |
| DB                    | 481 | TTTCTCTCTCCAGAGATGACAACTGCGCTCTTCTCCAGGCCCTTACGTGCCAATGC    | 540           |           |              |
| QY                    | 548 | TGTGACAGGAGCGCGCTCGATACGATGCTCGGTGCGAGGCTGCAAGTGTCTGA       | 607           |           |              |
| DB                    | 541 | TGTGACAGGAGCGCGCTCGATACGATGCTCGGTGCGAGGCTGCAAGTGTCTGA       | 600           |           |              |
| QY                    | 608 | GAAATCATGAAACAACTCAGTGGCTTAATCAAGCTTGAGATTTATATCCAGGACAA    | 667           |           |              |
| DB                    | 601 | GAAATCATGAAACAACTCAGTGGCTTAATCAAGCTTGAGATTTATATCCAGGACAA    | 660           |           |              |
| QY                    | 668 | CATGAAGAAAGATGTAGAGATACAGAGATGACAGTACAGAACAGCGCTGTGAT       | 727           |           |              |
| DB                    | 661 | CATGAAGAAAGATGTAGAGATACAGAGATGACAGTACAGAACAGCGCTGTGAT       | 720           |           |              |
| QY                    | 728 | GATGAAGATAGGAAACACTGTTGAACCAACAGCTGACCAACCGGAGTTAACTGA      | 787           |           |              |
| DB                    | 721 | GATGAAGATAGGAAACACTGTTGAAACCAACAGCTGACCAACCGGAGTTAACTGA     | 780           |           |              |
| QY                    | 788 | TGTGGAAGCCCAAGTATTAATCAGACCAAGACTTTGAACCTTCAGCTCTTGGAACTC   | 847           |           |              |
| DB                    | 781 | TGTGGAAGCCCAAGTATTAATCAGACCAAGACTTTGAACCTTCAGCTCTTGGAACTC   | 840           |           |              |
| QY                    | 848 | CCTCTCGAACAAATTTGGAAACAGATTTTGGACCGACGACAGTGAATAAACAAT      | 907           |           |              |

|    |      |  |      |  |  |
|----|------|--|------|--|--|
| DB | 841  | CTCTCGACAAACAATTTGGAAACAGATTTTGGACCGACGAGTGAATAAACAAT            | 900  |  |  |
| QY | 908  | GCAAGATAAGAACAGTTTCTAGAAAGAGTGCTAGTATGGAAGACAGACATCAT            | 967  |  |  |
| DB | 901  | GCAAGATAAGAACAGTTTCTAGAAAGAGTGCTAGTATGGAAGACAGACATCAT            | 960  |  |  |
| QY | 968  | CCACTACTAGTCAATAAAGAGAGAGACAGTACAGTACAGGTGTAGTATCCAAAGCAAA       | 1027 |  |  |
| DB | 961  | CCAACTACAGTCAATAAAGAGAGAGACAGTACAGTACAGGTGTAGTATCCAAAGCAAA       | 1020 |  |  |
| QY | 1028 | TTCCATCATTTGAAGAACTAGAAAAAATAGTGACTGCCACCGTGAATAATTCAGTTCT       | 1087 |  |  |
| DB | 1021 | TTCCATCATTTGAAGAACTAGAAAAAATAGTGACTGCCACCGTGAATAATTCAGTTCT       | 1080 |  |  |
| QY | 1088 | TCAAAAGCAGCAACATGATCTCATGAGACAGTTAATACTTACTGATATGATCCAC          | 1147 |  |  |
| DB | 1081 | TCAAAAGCAGCAACATGATCTCATGAGACAGTTAATACTTACTGATATGATCCAC          | 1140 |  |  |
| QY | 1148 | ATCAAACTCAGCTTAAGGACCCCACTGTTGCTTAAAGAGAACAAATCAGCTTCAGAGACTG    | 1207 |  |  |
| DB | 1141 | ATCAAACTCAGCTTAAGGACCCCACTGTTGCTTAAAGAGAACAAATCAGCTTCAGAGACTG    | 1200 |  |  |
| QY | 1208 | TGCTGAAGTATTCAAATCAGGACACACCAAAATGCGATCTACACGTTAACTTCCCTAA       | 1267 |  |  |
| DB | 1201 | TGCTGAAGTATTCAAATCAGGACACACCAAAATGCGATCTACACGTTAACTTCCCTAA       | 1260 |  |  |
| QY | 1268 | TTCTCAGAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAGAGCGGGTGGACAAT         | 1327 |  |  |
| DB | 1261 | TTCTCAGAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAGAGCGGGTGGACAAT         | 1320 |  |  |
| QY | 1328 | TATTCAGCGAGTGGAGATGGAGCGTTGATTTTTCAGAGGACTTGGAAAGATATAAGT        | 1387 |  |  |
| DB | 1321 | TATTCAGCGAGTGGAGATGGAGCGTTGATTTTTCAGAGGACTTGGAAAGATATAAGT        | 1380 |  |  |
| QY | 1388 | GGGATTTGGTAAACCCCTTCAGGAGAAATATGCGCTGGGAAATGAGTTTTCGCAACTGAC     | 1447 |  |  |
| DB | 1381 | GGGATTTGGTAAACCCCTTCAGGAGAAATATGCGCTGGGAAATGAGTTTTCGCAACTGAC     | 1440 |  |  |
| QY | 1448 | TAACTCAGCAACCGTATGTGCTTAAATAACACCTTAAAGACTGGGAAGGGAATGAGGCTTA    | 1507 |  |  |
| DB | 1441 | TAACTCAGCAACCGTATGTGCTTAAATAACACCTTAAAGACTGGGAAGGGAATGAGGCTTA    | 1500 |  |  |
| QY | 1508 | CTCAATGTATGAACATTTCTCTCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA      | 1567 |  |  |
| DB | 1501 | CTCAATGTATGAACATTTCTCTCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA      | 1560 |  |  |
| QY | 1568 | AGGACTTACAGGACAGCGCGCAAAATAGCAGCATCAGCAACCCAGGAAATGATTTAG        | 1627 |  |  |
| DB | 1561 | AGGACTTACAGGACAGCGCGCAAAATAGCAGCATCAGCAACCCAGGAAATGATTTAG        | 1620 |  |  |
| QY | 1628 | CACAAAGGATGGAGACAAACGACAAATGTATTTGCAAAATGTTTCAAAATGCTTAAACAGGAGG | 1687 |  |  |
| DB | 1621 | CACAAAGGATGGAGACAAACGACAAATGTATTTGCAAAATGTTTCAAAATGCTTAAACAGGAGG | 1680 |  |  |
| QY | 1688 | CTGGTGGTTTGTATGTCATGTCCTTCCAACTTGAACCGGAATGTACTATCCACAGAGGCA     | 1747 |  |  |
| DB | 1681 | CTGGTGGTTTGTATGTCATGTCCTTCCAACTTGAACCGGAATGTACTATCCACAGAGGCA     | 1740 |  |  |
| QY | 1748 | GAAACAAATAAGTTCAAAGGCAATTAATGCTACTGGAAGGCTCAGGCTATTCGCT          | 1807 |  |  |
| DB | 1741 | GAAACAAATAAGTTCAAAGGCAATTAATGCTACTGGAAGGCTCAGGCTATTCGCT          | 1800 |  |  |
| QY | 1808 | CAAGGCCCAACCAATGATGATCCGACAGCAGATTTTCTAAACATCCCACTCAGG           | 1867 |  |  |
| DB | 1801 | CAAGGCCCAACCAATGATGATCCGACAGCAGATTTTCTAAACATCCCACTCAGG           | 1860 |  |  |
| QY | 1868 | AACGTGTCGAACTATTTTCAAGACTTAAGCCAGTGCACTGAAAGTCAAGGCTGCGCA        | 1927 |  |  |
| DB | 1861 | AACGTGTCGAACTATTTTCAAGACTTAAGCCAGTGCACTGAAAGTCAAGGCTGCGCA        | 1920 |  |  |
| QY | 1928 | CTGTGCTCTTCCACCAAGAGGGGCTGTGCTCGGTGCTGACGGGACCCACATGCTCCA        | 1987 |  |  |

|    |   |
|----|---|
| CC | and preventing HGD and cancer, and in gene therapy. The present sequence encodes human Tie2 ligand2, which is used in the exemplification of the present invention. The human Tie2 ligand2 gene is located on chromosome 8. |
| CC | 8.  |
| CC |   |
| XX |   |
| SQ | Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;   |
|    | Query Match 99.4%; Score 2269; DB 12; Length 2269;  |
|    | Best Local Similarity 100.0%; Pred. No. 0;  |
|    | Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   |
| QY | 8 TGGGTTGGTGTATTATCTCTCTCCAGCCCTTGAGGGAGGGAACAACACTGTAGAGTCTTGGGG 67  |
| DB | 1 TGGGTTGGTGTATTATCTCTCTCCAGCCCTTGAGGGAGGGAACAACACTGTAGAGTCTTGGGG 60  |
| QY | 68 AGAGAGGACAAGAAGCCGCTGAAAGCTGCTCTGTTAAAGCTGCACACAGCCCTCCCAAGTG 127  |
| DB | 61 AGAGAGGACAAGAAGCCGCTGAAAGCTGCTCTGTTAAAGCTGCACACAGCCCTCCCAAGTG 120  |
| QY | 128 AGCAGGACTGTTCTTCCCACTGCAATCTGCAGTTTACTGCATGCCCTGGAGAGAAACAACAG 187  |
| DB | 121 AGCAGGACTGTTCTTCCCACTGCAATCTGCAGTTTACTGCATGCCCTGGAGAGAAACAACAG 180  |
| QY | 188 CAGTAAAAACAGGTTTGCTACTGAAAAAGAGAGAAAGAGAGAGTCTTTCATTTGACGGACC 247   |
| DB | 181 CAGTAAAAACAGGTTTGCTACTGAAAAAGAGAGAAAGAGAGAGTCTTTCATTTGACGGACC 240   |
| QY | 248 CAGCCATGGCAGCGTAGCAGCCCTGCGTTTCAGACGGCAGCAGCTCGGAGCTCTGGAAGT 307  |
| DB | 241 CAGCCATGGCAGCGTAGCAGCCCTGCGTTTCAGACGGCAGCAGCTCGGAGCTCTGGAAGT 300  |
| QY | 308 GTGTTTGGCCCTCAAGTTTGGCTAAGCTGCTGGTTTTATTACTGAAGAAAGAAATGTGGCAGAT 367  |
| DB | 301 GTGTTTGGCCCTCAAGTTTGGCTAAGCTGCTGGTTTTATTACTGAAGAAAGAAATGTGGCAGAT 360  |
| QY | 368 TGTGTTTCTTATCTCTGAGCTGTGATCTTGTGTCGCGCAGCCCTATAACAACTTTTCGGAA 427   |
| DB | 361 TGTGTTTCTTATCTCTGAGCTGTGATCTTGTGTCGCGCAGCCCTATAACAACTTTTCGGAA 420   |
| QY | 428 GAGCATGACAGCATAGGAAAGAGCAATATCAGGTCCAGCTGGGTCCCTGCGAGCTACAC 487   |
| DB | 421 GAGCATGACAGCATAGGAAAGAGCAATATCAGGTCCAGCTGGGTCCCTGCGAGCTACAC 480   |
| QY | 488 TTTTCCTCTCTGCGCAGAGATGGAACAACCTGCGCTCTTCTCTCCAGCCCTTACGTGTCCAATGC 547   |
| DB | 481 TTTTCCTCTCTGCGCAGAGATGGAACAACCTGCGCTCTTCTCTCCAGCCCTTACGTGTCCAATGC 540   |
| QY | 548 TGTGAGAGGGACGCGCGCTCGAATACGATGACTCTGCGTGAGAGGCTGCAAGTGTCTGGA 607  |
| DB | 541 TGTGAGAGGGACGCGCGCTCGAATACGATGACTCTGCGTGAGAGGCTGCAAGTGTCTGGA 600  |
| QY | 608 GAACATCATGGAAGAACACACTCAGTGGCTTAATGAAGCTTGAAGTATATATCCAGGACAA 667   |
| DB | 601 GAACATCATGGAAGAACACACTCAGTGGCTTAATGAAGCTTGAAGTATATATCCAGGACAA 660   |
| QY | 668 CATGAAGAAAGAAATGGTAGAGATACAGCAGAATGCAAGTACAGAACCCAGACGGCTGTGAT 727  |
| DB | 661 CATGAAGAAAGAAATGGTAGAGATACAGCAGAATGCAAGTACAGAACCCAGACGGCTGTGAT 720  |
| QY | 728 GATAGAAATAGGGACAAACCTGTTGAACCCAAAACAGCTTGAGCAAAACGCGGAAGTTTAACATGA 787  |
| DB | 721 GATAGAAATAGGGACAAACCTGTTGAACCCAAAACAGCTTGAGCAAAACGCGGAAGTTTAACATGA 780  |
| QY | 788 TGTGGAAGCCCAAGTATTAAATCAGACCAAGAGACTTGAACCTTCAGCTCTTGGAAACATC 847   |
| DB | 781 TGTGGAAGCCCAAGTATTAAATCAGACCAAGAGACTTGAACCTTCAGCTCTTGGAAACATC 840   |
| QY | 848 CCTCTCGCAACAACTTGGAAAAACAGATTTTTCGACAGACCAAGTCAAAATAAACAAATT 907  |
| DB | 841 CCTCTCGCAACAACTTGGAAAAACAGATTTTTCGACAGACCAAGTCAAAATAAACAAATT 900  |
| QY | 908 GCAAGATAAGCAAGTTCCTTAGAAAAAGAGGTCCTAGCTATGGAAGACAAGCAATCAT 967  |



|    |     |   |  |
|----|-----|---|--|
| XX | SQ  | Sequence  | 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other; |
|    |     | Query Match   | 99.4%; Score 2269; DB 12; Length 2269;             |
|    |     | Best Local Similarity   | 100.0%; Pred. No. 0;                               |
|    |     | Matches 2269; Conservative                                      | 0; Mismatches 0; Indels 0; Gaps 0;                 |
| QY | 8   | TGGGTTGGTGTATTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTATAGGATCTGGGG   | 67   |
| DB | 1   | TGGGTTGGTGTATTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTATAGGATCTGGGG   | 60   |
| QY | 68  | AGAGAGAAACAAGCAACCGTGAAGCTGCTCTGTAAAGCTGCACACAGCCCTCCCAAGTG     | 127  |
| DB | 61  | AGAGAGNAANAAGCAACCGTGAAGCTGCTCTGTAAAAGCTGCACACAGCCCTCCCAAGTG    | 120  |
| QY | 128 | AGCAGGACTGTTCCTCCCACTGCAATCTGACAGTTTTACTGCATGCCCTGGAGAGAACAACAG | 187  |
| DB | 121 | AGCAGGACTGTTCCTCCCACTGCAATCTGACAGTTTTACTGCATGCCCTGGAGAGAACAACAG | 180  |
| QY | 188 | CAGTAATAAACCAGGTTTGTCTACTGGAAAAAGAGAGAGAGAACATTTCTATGACGGACC    | 247  |
| DB | 181 | CAGTAATAAACCAGGTTTGTCTACTGGAAAAAGAGAGAGAGAACATTTCTATGACGGACC    | 240  |
| QY | 248 | CAGCCATGGCAGCGTAGCACGCCCTGCGCTTTTCAGACGGCAGCAGCTCGGGACTCTGGACGT | 307  |
| DB | 241 | CAGCCATGGCAGCGTAGCACGCCCTGCGCTTTTCAGACGGCAGCAGCTCGGGACTCTGGACGT | 300  |
| QY | 308 | GTGTTTGGCCCTCAAGTTTGTCTAGCTGCTCGTTTATTACTGAAGAAAGATGTGGCAGAT    | 367  |
| DB | 301 | GTGTTTGGCCCTCAAGTTTGTCTAGCTGCTCGTTTATTACTGAAGAAAGATGTGGCAGAT    | 360  |
| QY | 368 | TGTTTTCTTTACTCTGAGCTGTGATCTTGCTTGGCCGCGACGCTATAAACAACTTTTCGGAA  | 427  |
| DB | 361 | TGTTTTCTTTACTCTGAGCTGTGATCTTGCTTGGCCGCGACGCTATAAACAACTTTTCGGAA  | 420  |
| QY | 428 | GAGCATGGAACAGCATAGAAAGAAAGCAATATACGGTCCAGCATGGGCTCTGCAGCTACAC   | 487  |
| DB | 421 | GAGCATGGAACAGCATAGAAAGAAAGCAATATACGGTCCAGCATGGGCTCTGCAGCTACAC   | 480  |
| QY | 488 | TTTTCTCTCCAGAGATGGACAACTCGCGCTCTTCCTCCAGCCCCCTACGCTGTCCTAATGC   | 547  |
| DB | 481 | TTTTCTCTCCAGAGATGGACAACTCGCGCTCTTCCTCCAGCCCCCTACGCTGTCCTAATGC   | 540  |
| QY | 548 | TGTGCAGAGGACGCGCGCTCGAATACGATGACTCGGTGCAGAGGCTCGAAGTGTCTGGA     | 607  |
| DB | 541 | TGTGCAGAGGACGCGCGCTCGAATACGATGACTCGGTGCAGAGGCTCGAAGTGTCTGGA     | 600  |
| QY | 608 | GAACATCATGGMAAACAACTCAGTGGCTTAANTAGCTTGAGNATTTATCCAGACAA        | 667  |
| DB | 601 | GAACATCATGGMAAACAACTCAGTGGCTTAANTAGCTTGAGNATTTATATCCAGACAA      | 660  |
| QY | 668 | CATGAAGAAAGAAATGTTAGAGATACAGCAGAAATGCAGTACAGAAACAGACGCGCTGTGAT  | 727  |
| DB | 661 | CATGAAGAAAGAAATGTTAGAGATACAGCAGAAATGCAGTACAGAAACAGACGCGCTGTGAT  | 720  |
| QY | 728 | GATAGAAATAGGACAAACCTGTTTGAACCAAACAGCTGAGCAAAACGCGGAAGTTAACTGA   | 787  |
| DB | 721 | GATAGAAATAGGACAAACCTGTTTGAACCAAACAGCTGAGCAAAACGCGGAAGTTAACTGA   | 780  |
| QY | 788 | TGTGGAGGCCCAAGTATTTAAATCAGACCAAGACTTTGAACTTTCAGCTCTTTCGAAACATC  | 847  |
| DB | 781 | TGTGGAGGCCCAAGTATTTAAATCAGACCAAGACTTTGAACTTTCAGCTCTTTCGAAACATC  | 840  |
| QY | 848 | CCTCTCGACAAACAAATTTGAAAAACAGATTTTGGACCCAGACCAAGTGAATAAACAAAT    | 907  |
| DB | 841 | CCTCTCGACAAACAAATTTGAAAAACAGATTTTGGACCCAGACCAAGTGAATAAACAAAT    | 900  |
| QY | 908 | GCAGATAAGAACAGTTTTCCTAGAAAGAGAGGTGCTAGCTATGGAAGACCAAGCACATCAT   | 967  |
| DB | 901 | GCAGATAAGAACAGTTTTCCTAGAAAGAGAGGTGCTAGCTATGGAAGACCAAGCACATCAT   | 960  |
| QY | 968 | CCAACCTACAGTCAATAAAGAGAGAAAGATCAAGTCAAGGCTGTATATCCAAAGCAAAA     | 1027   |



QY 2108 GAATCAGACTGACAGTTTACAGACGCTGCTGTCTCAACCAAGAAATGTTATGTGCAAGTTT 2167  
DB 2101 GAATCAGACTGACAGTTTACAGACGCTGCTGTCTCAACCAAGAAATGTTATGTGCAAGTTT 2160  
QY 2168 ATCAGTAATAACTGGAAGAACAGACATTTATGTTATACATACAGATCATCTTGAACCT 2227  
DB 2161 ATCAGTAATAACTGGAAGAACAGACATTTATGTTATACATACAGATCATCTTGAACCT 2220  
QY 2228 GCATTCTCTGACACTGTTTATACACTGTGTAATACCCATATGTCCT 2276  
DB 2221 GCATTCTCTGACACTGTTTATACACTGTGTAATACCCATATGTCCT 2269

## RESULT 14

ADS13801

ID ADS13801 standard; DNA; 2269 BP.

XX AC ADS13801;

XX DT 02-DEC-2004 (first entry)

XX DE Human angiotensin-2 (Ang-2) encoding DNA.

XX KW Ang-1; extracellular matrix; ECM; angiotensin; cytostatic; vasotropic;  
XX KW anti-diabetic; anti-arthritis; cerebroprotective; anti-angiogenic;  
XX KW gene therapy; human; gene; Ang-2; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 350..1940

XX FT /\*tag= a

XX FT /product= "Ang-2"

XX PN WO2004076650-A2.

XX PD 10-SEP-2004.

XX PF 27-FEB-2004; 2004WO-US006101.

XX PR 27-FEB-2003; 2003US-0450592P.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Yu Q;

XX PS WPI; 2004-653413/63.

XX DR P-PSDB; ADS13783.

XX PT New pharmaceutical composition comprises a pharmaceutical carrier and an  
XX PT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein  
XX PT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or  
XX PT ischemia.

XX PS Disclosure; SEQ ID NO 33; 114pp; English.

XX CC The invention relates to a pharmaceutical composition comprising a  
XX CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-  
XX CC binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also  
XX CC provided are methods of treating an individual suspected of having  
XX CC coronary artery disease, vascular disease or a condition involving  
XX CC ischemia; of promoting angiogenesis, endothelial survival and  
XX CC maintaining vascular integrity in an individual; of treating an  
XX CC individual suspected of having a disease related to lack of blood vessels  
XX CC to effectively promote angiogenesis in the patients with the diseases  
XX CC related to lack of blood vessels such as ischemia in hearts and limbs;  
XX CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,  
XX CC atherosclerosis risk by maintaining the health and integrity of blood  
XX CC vessels; to assist the recovery of the patients who had stroke and the  
XX CC angioplasty procedure by promoting the growth/survival of endothelial  
XX CC cells and establish endothelial monolayer and inhibit excessive  
XX CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;

CC to treat patients with restenosis by inhibiting re-closure of blood  
CC vessel after inserting stents into blood vessels; to make stable and  
CC functional artificial blood vessels comprising using the composition  
CC above; of identifying compounds that modulates binding of Ang-1 to ECM;  
CC of treating an individual suspected of having cancer; of preventing  
CC diabetes and/or arthritis in an individual suspected of being at risk of  
CC developing diabetes or arthritis. The pharmaceutical composition is  
CC useful for treating diseases and disorders, e.g. cancer, coronary artery  
CC disease, vascular disease, ischemia, restenosis, diabetes, stroke,  
CC angiogenesis, or arthritis. The present sequence represents the human Ang  
CC -2 encoding DNA.

XX SQ Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;

Query Match 99.4%; Score 2269; DB 13; Length 2269;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGGTTGGTGTATCTCTCCAGCCTTGAGGAGGGGACACACTGTAGGATCTGGGG 67

DB 1 TGGGTTGGTGTATCTCTCCAGCCTTGAGGAGGGGACACACTGTAGGATCTGGGG 60

QY 68 AGAGAGGAACAAGGACCGTGAAGCTCTCTAAAGCTGACAGAGCCCTCCCAAGTG 127

DB 61 AGAGAGGAACAAGGACCGTGAAGCTCTCTAAAGCTGACAGAGCCCTCCCAAGTG 120

QY 128 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTCTTACTGCTGGAGAGAACAG 187

DB 121 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTCTTACTGCTGGAGAGAACAG 180

QY 188 CAGTAAACCAGGTTTGTCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 247

DB 181 CAGTAAACCAGGTTTGTCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

QY 248 CAGCCATGCGAGCTAGCAGCCCTGCGTTTTCAGACGCGCAGCTCGGGACTCTGACGT 307

DB 241 CAGCCATGCGAGCTAGCAGCCCTGCGTTTTCAGACGCGCAGCTCGGGACTCTGACGT 300

QY 308 GTGTTTGCCTCAAGTTTGTCTGAGTCTGCTGTTTATTACTGAAGAAGAGAGAGAGAG 367

DB 301 GTGTTTGCCTCAAGTTTGTCTGAGTCTGCTGTTTATTACTGAAGAAGAGAGAGAGAG 360

QY 368 TGTGTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCGGAGCCTATACAACTTTCGGA 427

DB 361 TGTGTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCGGAGCCTATACAACTTTCGGA 420

QY 428 GAGCATGGACAGCATAGGAAGAGCAATATCAGGTCCAGCTGGGTCTCGAGCTACAC 487

DB 421 GAGCATGGACAGCATAGGAAGAGCAATATCAGGTCCAGCTGGGTCTCGAGCTACAC 480

QY 488 TTTCTCTCTGCCAGAGATGACAACTGCCGCTCTTCTCCAGGCCCTTACGTGTCCAATGC 547

DB 481 TTTCTCTCTGCCAGAGATGACAACTGCCGCTCTTCTCCAGGCCCTTACGTGTCCAATGC 540

QY 548 TGTGCGAGAGGAGCGCGCGCTCGAATACGATGACTCGGTGCGAGAGGCTGCAAGTCTGGA 607

DB 541 TGTGCGAGAGGAGCGCGCGCTCGAATACGATGACTCGGTGCGAGAGGCTGCAAGTCTGGA 600

QY 608 GAACATCATGGAAGAGCAACACTCAGTGGCTTAATGAAGCTTGAAGATTTATATCCAGGACAA 667

DB 601 GAACATCATGGAAGAGCAACACTCAGTGGCTTAATGAAGCTTGAAGATTTATATCCAGGACAA 660

QY 668 CATGAAGAAGAAATGTTAGAGATACAGCAAGATGCAAGTACAGAACCCAGACGGCTGTGAT 727

DB 661 CATGAAGAAGAAATGTTAGAGATACAGCAAGATGCAAGTACAGAACCCAGACGGCTGTGAT 720

QY 728 GATAGAAATAGGAGCAAACTCTGTTGAACCAAACTGAGCAAAACCGCGGAAGTTAATGA 787

DB 721 GATAGAAATAGGAGCAAACTCTGTTGAACCAAACTGAGCAAAACCGCGGAAGTTAATGA 780

QY 788 TGTGGAAGCCCAAGTATTAAATCAGACCCAGAGACTTGAAGTTCAGCTCTTGGAACTC 847

DB 781 TGTGGAAGCCCAAGTATTAAATCAGACCCAGAGACTTGAAGTTCAGCTCTTGGAACTC 840

QY 848 CCTCTCGACAAACAAATTGGAAAAACAGATTTTGGACAGACACAGTGGAATATAACAAAT 907  
DB |||||  
QY 841 CCTCTCGACAAACAAATTGGAAAAACAGATTTTGGACAGACACAGTGGAATATAACAAAT 900  
DB |||||  
QY 908 GCAAGATAGAACAGTTTCTTCTAGAAAAAGAGTGCTAGCTATGGAAGACAACATCAT 967  
DB |||||  
QY 901 GCAAGATAGAACAGTTTCTTCTAGAAAAAGAGTGCTAGCTATGGAAGACAACATCAT 960  
DB |||||  
QY 968 CCAACTACAGTCAATAAAGAGAGAGAGATCAGCTACAGGTGTAGTATCAAGCAAAA 1027  
DB |||||  
QY 961 CCAACTACAGTCAATAAAGAGAGAGAGATCAGCTACAGGTGTAGTATCAAGCAAAA 1020  
DB |||||  
QY 1028 TTCCATCATTTGAAGAACTAGAAAAAATAAGTAGTCTGCCACGGTGAATAATTCAGTTCT 1087  
DB |||||  
QY 1021 TTCCATCATTTGAAGAACTAGAAAAAATAAGTAGTCTGCCACGGTGAATAATTCAGTTCT 1080  
DB |||||  
QY 1088 TCAAAAGCAGCAACATGATCTCATGGAGACATTAATAATTTACTGATGATGTCAC 1147  
DB |||||  
QY 1081 TCAAAAGCAGCAACATGATCTCATGGAGACATTAATAATTTACTGATGATGTCAC 1140  
DB |||||  
QY 1148 ATCAAACTCAGCTAAGGACCCCACTGTTGCTAAAGAGAACAAATCAGCTTCAGAGACTG 1207  
DB |||||  
QY 1141 ATCAAACTCAGCTAAGGACCCCACTGTTGCTAAAGAGAACAAATCAGCTTCAGAGACTG 1200  
DB |||||  
QY 1208 TGCTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTACAGCTTAAACATTCCTTAA 1267  
DB |||||  
QY 1201 TGCTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTACAGCTTAAACATTCCTTAA 1260  
DB |||||  
QY 1268 TTCTACAGAAAGATCAAGCCCTACTGTGACATGGAAGCTGGAGGCGGTGACAAAT 1327  
DB |||||  
QY 1261 TTCTACAGAAAGATCAAGCCCTACTGTGACATGGAAGCTGGAGGCGGTGACAAAT 1320  
DB |||||  
QY 1328 TATTTCAGGACGTGAGGATGGCAGCGTTGATTTTTCAGAGGACTTGAAGAGATATAAGT 1387  
DB |||||  
QY 1321 TATTTCAGGACGTGAGGATGGCAGCGTTGATTTTTCAGAGGACTTGAAGAGATATAAGT 1380  
DB |||||  
QY 1388 GGGATTTGGTAAACCTTCAGGAGAAATATTTGGCTGGGAATAGTTTGTTCGCAACTGAC 1447  
DB |||||  
QY 1381 GGGATTTGGTAAACCTTCAGGAGAAATATTTGGCTGGGAATAGTTTGTTCGCAACTGAC 1440  
DB |||||  
QY 1448 TAAATCAGCAACCGTATGTGCTTAAATAACACTTAAAGCTGGGAAGGAATGAGGCTTA 1507  
DB |||||  
QY 1441 TAAATCAGCAACCGTATGTGCTTAAATAACACTTAAAGCTGGGAAGGAATGAGGCTTA 1500  
DB |||||  
QY 1508 CTCATTGTATGAACATTTCTATCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1567  
DB |||||  
QY 1501 CTCATTGTATGAACATTTCTATCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1560  
DB |||||  
QY 1568 AGGACTTACAGGACAGCGCGCAAAATAAGCAGCATCAGCCCAACAGGAAATGATTTTAG 1627  
DB |||||  
QY 1561 AGGACTTACAGGACAGCGCGCAAAATAAGCAGCATCAGCCCAACAGGAAATGATTTTAG 1620  
DB |||||  
QY 1628 CACAAAGGATGAGACAACGACAAATGTATTTGCAAAATGTTTCAAAATGCTTAACAGGAG 1687  
DB |||||  
QY 1621 CACAAAGGATGAGACAACGACAAATGTATTTGCAAAATGTTTCAAAATGCTTAACAGGAG 1680  
DB |||||  
QY 1688 CTGGTGGTTTGTATGATGTGCTTCCAACTTGAACCGAATGTACTATCCACAGGCA 1747  
DB |||||  
QY 1681 CTGGTGGTTTGTATGATGTGCTTCCAACTTGAACCGAATGTACTATCCACAGGCA 1740  
DB |||||  
QY 1748 GAACACAAATAGTTTCAACGGCATTAATTTGTTACTTGAAGAGGCTCAGGCTATTTCGT 1807  
DB |||||  
QY 1741 GAACACAAATAGTTTCAACGGCATTAATTTGTTACTTGAAGAGGCTCAGGCTATTTCGT 1800  
DB |||||  
QY 1808 CAAGGCAACCAATGATGATCCGACAGCATTTCTAAACATCCAGTCCACCTGAGG 1867  
DB |||||  
QY 1801 CAAGGCAACCAATGATGATCCGACAGCATTTCTAAACATCCAGTCCACCTGAGG 1860  
DB |||||  
QY 1868 TACTGCTCGAACTATTTTCAAGACTTAAGCCAGTGCACGTAAGTACCGGCTGCGCA 1927  
DB |||||  
QY 1861 TACTGCTCGAACTATTTTCAAGACTTAAGCCAGTGCACGTAAGTACCGGCTGCGCA 1920  
DB |||||

QY 1928 CTGTGCTCTCTTCCACCAAGAGGCGGTGTGTCTGGTGTGACGGGACCCACATGCTCCA 1987  
DB |||||  
QY 1921 CTGTGCTCTCTTCCACCAAGAGGCGGTGTGTCTGGTGTGACGGGACCCACATGCTCCA 1980  
DB |||||  
QY 1988 GATTAGAGCCTGTAAACTTTATCACTTAAACTTTGATCACTTAAACGGACCAAGCAAGAC 2047  
DB |||||  
QY 1981 GATTAGAGCCTGTAAACTTTATCACTTAAACTTTGATCACTTAAACGGACCAAGCAAGAC 2040  
DB |||||  
QY 2048 CCTAAACATCCATAATTTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA 2107  
DB |||||  
QY 2041 CCTAAACATCCATAATTTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA 2100  
DB |||||  
QY 2108 GAATCAGACTGACAGTTTACAGACGCTGTCACACCAAGAAATTTATGTCGAAGTTT 2167  
DB |||||  
QY 2101 GAATCAGACTGACAGTTTACAGACGCTGTCACACCAAGAAATTTATGTCGAAGTTT 2160  
DB |||||  
QY 2168 ATCAGTAAATACTGGAAAAACAGACACTTATGTTATACATAACAGATCATCTTGAAC 2227  
DB |||||  
QY 2161 ATCAGTAAATACTGGAAAAACAGACACTTATGTTATACATAACAGATCATCTTGAAC 2220  
DB |||||  
QY 2228 GCATTTCTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCT 2276  
DB |||||  
QY 2221 GCATTTCTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCT 2269  
DB |||||  
RESULT 15  
ABX63023  
ID ABX63023 standard; cDNA; 2384 BP.  
XX  
AC ABX63023;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Human cDNA #23 differentially expressed in activated vascular tissue.  
XX  
KW Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiac; hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective; gene therapy; vascular disease; cancer; coronary; artery disease; hypertension; diabetes; pre-eclampsia; restenosis; ischaemia-reperfusion injury; stroke.  
XX  
OS Homo sapiens.  
XX  
PN US2002137081-A1.  
XX  
PD 26-SEP-2002.  
XX  
PF 08-JAN-2002; 2002US-00044090.  
XX  
PR 28-JUL-2000; 2000US-0222469P.  
PR 08-JAN-2001; 2001US-0260483P.  
XX  
PA (BAND/) BANDMAN O.  
XX  
PI Bandman O;  
XX  
DR WPI; 2003-110597/10.  
XX  
PT Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated vascular tissue.  
XX  
PS Claim 1; Page; 18pp; English.  
XX  
CC This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have antiarteriosclerotic; cytostatic; cardiac; hypotensive; antidiabetic; gynaecological; vasotropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high-throughput methods for detecting differential expression of one or more

cDNAs in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a cDNA of the invention. A protein encoded by the cDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or recombinant protein from a sample. The nucleotides may be useful for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion injury, restenosis, or stroke. The cDNAs can also be used for large-scale genetic or gene expression analysis of several new nucleic acid molecules. Antibodies to the proteins encoded by the cDNAs are useful for diagnosing pre-pathologic disorders, and chronic or acute diseases associated with abnormalities in the expression, amount or distribution of the protein. The present sequence represents a cDNA of the invention that is differentially expressed in activated vascular tissue. Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from USPTO at <http://sequences.uspto.gov/sequence.html?docID=20020137081>

Sequence 2384 BP; 797 A; 508 C; 533 G; 546 T; 0 U; 0 Other;

Query Match 97.9%; Score 2233.6; DB 8; Length 2384;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2239; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

|    |     |              |          |       |        |        |          |        |        |          |            |         |            |            |            |           |        |             |        |          |
|----|-----|--------------|----------|-------|--------|--------|----------|--------|--------|----------|------------|---------|------------|------------|------------|-----------|--------|-------------|--------|----------|
| Qy | 35  | TTGAGGAGGGAA | CAA      | CAC   | TGT    | AGAT   | CTCGGG   | GAGAGG | ACAA   | AGGACCGT | GAAAGCT    | 94      |            |            |            |           |        |             |        |          |
| Db | 9   | TTGATTCGGAT  | TACTG    | ACACT | GTAGG  | ATCTG  | GGGAGAGG | AGAA   | CAAA   | GGAGCCGT | GAAAGCT    | 68      |            |            |            |           |        |             |        |          |
| Qy | 95  | GCTCTGTA     | AAAGCTG  | ACAC  | CAG    | CCCTCC | CAAGTG   | ACGAG  | CACTGT | TCTTCC   | CACTGCAATC | 154     |            |            |            |           |        |             |        |          |
| Db | 69  | GCCTGT       | TAAAGCTG | ACAC  | AGCCCT | CCCA   | AGTG     | ACGAG  | CACTGT | TCTTCC   | CACTGCAATC | 128     |            |            |            |           |        |             |        |          |
| Qy | 155 | TGACAG       | TTTACT   | CTG   | ATGCT  | CGAG   | AGAA     | CA     | CAG    | CAGT     | AAAA       | CCAG    | TTTGTCTACT | 214        |            |           |        |             |        |          |
| Db | 129 | TGACAG       | TTTACT   | CG    | ATGCT  | CGAG   | AGAA     | CA     | CAG    | CAGT     | AAAA       | CCAG    | TTTGTCTACT | 214        |            |           |        |             |        |          |
| Qy | 215 | AAAGAG       | AAAGAG   | AGAG  | ACTTT  | CA     | TGAC     | GGAC   | CCCA   | GCCAT    | GGC        | AGCTAG  | CAGCCCTG   | CG 274     |            |           |        |             |        |          |
| Db | 189 | AAAGAG       | AAAGAG   | AGAG  | ACTTT  | CA     | TGAC     | GGAC   | CCCA   | GCCAT    | GGC        | AGCTAG  | CAGCCCTG   | CG 248     |            |           |        |             |        |          |
| Qy | 275 | TTTCAG       | ACGG     | CAG   | CAGCT  | TC     | TGGA     | CGT    | GTGTT  | TGGCCCT  | CAAG       | TTTGTCT | TAAGCTG    | 334        |            |           |        |             |        |          |
| Db | 249 | TTTCAG       | ACGG     | CAG   | CAGCT  | TC     | TGGA     | CGT    | GTGTT  | TGGCCCT  | CAAG       | TTTGTCT | TAAGCTG    | 308        |            |           |        |             |        |          |
| Qy | 335 | CTG          | TTTATT   | ACT   | GA     | AAAA   | GAA      | TA     | TGG    | CAG      | ATTG       | TTTCTTT | TACTCT     | CTGAGCTGTG | ATCT 394   |           |        |             |        |          |
| Db | 309 | CTG          | TTTATT   | ACT   | GA     | AAAA   | GAA      | TA     | TGG    | CAG      | ATTG       | TTTCTTT | TACTCT     | CTGAGCTGTG | ATCT 368   |           |        |             |        |          |
| Qy | 395 | TGCT         | TGGCCG   | CAGCT | TAT    | NAC    | AACT     | TTTC   | GG     | AA       | GAGCAT     | TGG     | CAGCAT     | TAGGA      | AAAGCA 454 |           |        |             |        |          |
| Db | 369 | TGCT         | TGGCCG   | CAGCT | TAT    | NAC    | AACT     | TTTC   | GG     | AA       | GAGCAT     | TGG     | CAGCAT     | TAGGA      | AAAGCA 428 |           |        |             |        |          |
| Qy | 455 | ATAT         | CAGT     | CCAG  | ATGG   | TCT    | CG       | AGCT   | TAC    | ACT      | TTTCT      | CTCC    | AGAGAT     | GGACAA     | CTG 514    |           |        |             |        |          |
| Db | 429 | ATAT         | CAGT     | CCAG  | ATGG   | TCT    | CG       | AGCT   | TAC    | ACT      | TTTCT      | CTCC    | AGAGAT     | GGACAA     | CTG 488    |           |        |             |        |          |
| Qy | 515 | CCG          | CTTCT    | CTCC  | AG     | CCCT   | CA       | GTG    | CCAA   | TGCT     | GTG        | CAG     | AGG        | ACG        | CCCGCTG    | CAATA 574 |        |             |        |          |
| Db | 489 | CCG          | CTTCT    | CTCC  | AG     | CCCT   | CA       | GTG    | CCAA   | TGCT     | GTG        | CAG     | AGG        | ACG        | CCCGCTG    | CAATA 548 |        |             |        |          |
| Qy | 575 | CGAT         | GACT     | CCGT  | GC     | AG     | AGCT     | GC     | TA     | AGT      | GC         | TA      | AGT        | GC         | TA         | AGT 634   |        |             |        |          |
| Db | 549 | CGAT         | GACT     | CCGT  | GC     | AG     | AGCT     | GC     | TA     | AGT      | GC         | TA      | AGT        | GC         | TA         | AGT 608   |        |             |        |          |
| Qy | 635 | GCT          | AT       | GA    | AGCT   | TTG    | AGAA     | TTT    | AT     | TAT      | CCAG       | GA      | CAAC       | TGA        | AAAG       | AAAT      | TGTTAG | AGATACA 694 |        |          |
| Db | 609 | GCT          | AT       | GA    | AGCT   | TTG    | AGAA     | TTT    | AT     | TAT      | CCAG       | GA      | CAAC       | TGA        | AAAG       | AAAT      | TGTTAG | AGATACA 668 |        |          |
| Qy | 695 | GC           | AG       | AT    | CG     | AGT    | ACAG     | AA     | CC     | CA       | CGCT       | GTG     | AT         | TAG        | AAAA       | TAGG      | GA     | CAAA        | CCTGTT | AGAA 754 |

|    |      |  |      |
|----|------|--|------|
| QY | 1835 | AGCAGATTTCTAAACATCCAGTCCACCTGAGGAACTGTCTCGAACTATTTTCAAAGACT  | 1894 |
| Db | 1809 | AGCAGATTTCTAAACATCCAGTCCACCTGAGGAACTGTCTCGAACTATTTTCAAAGACT  | 1868 |
| QY | 1895 | TAAGCCAGTGCACCTGAAAGTCAAGGCTGCGGACCTGTGTCTCTCCACCAAGAGGGCG   | 1954 |
| Db | 1869 | TAAGCCAGTGCACCTGAAAGTCAAGGCTGCGGACCTGTGTCTCTCCACCAAGAGGGCG   | 1928 |
| QY | 1955 | TGTGCTCGGTGCTGACGGGACCCACATGCTCCAGATTAGAGCTGTAAACTTTTATCACTT | 2014 |
| Db | 1929 | TGTGCTCGGTGCTGACGGGACCCACATGCTCCAGATTAGAGCTGTAAACTTTTATCACTT | 1988 |
| QY | 2015 | AAACTTGCATCACTTAAACGACCAAGCAAGACCCCTAAACATCCATAATTGTGATTAGAC | 2074 |
| Db | 1989 | AAACTTGCATCACTTAAACGACCAAGCAAGACCCCTAAACATCCATAATTGTGATTAGAC | 2048 |
| QY | 2075 | AGAACACCTATGCAAGATGAACCCGAGGCTGAGAAATCAGACTGACAGTTTACAGACGCT | 2134 |
| Db | 2049 | AGAACACCTATGCAAGATGAACCCGAGGCTGAGAAATCAGACTGACAGTTTACAGACGCT | 2108 |
| QY | 2135 | GCTGTCAACAACCAAGAACTTTATGTGCAAGTTTATCAGTAAATAACTGGAAAAACAACA | 2194 |
| Db | 2109 | GCTGTCAACAACCAAGAACTTTATGTGCAAGTTTATCAGTAAATAACTGGAAAAACAACA | 2168 |
| QY | 2195 | CTTATGTTATACAATACAGATCATCTTGGAACTGCAATCTCTGAGCACTGTTTATACAC  | 2254 |
| Db | 2169 | CTTATGTTATACAATACAGATCATCTTGGAACTGCAATCTCTGAGCACTGTTTATACAC  | 2228 |
| QY | 2255 | TGTGTAATACCCATATGTCCTGAATTC                                  | 2282 |
| Db | 2229 | TGTGTAATACCCATATGTCCTGAATTC                                  | 2256 |

Search completed: July 29, 2005, 03:19:05  
Job time : 1311.44 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 02:36:24 ; Search time 8059.43 Seconds  
(without alignments)  
10777.765 Million cell updates/sec

Title: US-10-603-293-5

Perfect score: 2282

Sequence: 1 gaattctgggtgtgttt.....taccatattgtctgaattc 2282

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hcc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_ges1:\*

9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description        |
|------------|--------|-------------|--------|-------|--------------------|
| 1          | 2114.6 | 92.7        | 2134   | 3     | CR620685 full-leng |
| 2          | 2029.2 | 88.9        | 2083   | 3     | BC022490 Homo sapi |
| 3          | 1068.2 | 46.8        | 2443   | 3     | AK048622 Mus muscu |
| 4          | 1068.2 | 46.8        | 2475   | 3     | AK019860 Mus muscu |
| 5          | 933.4  | 40.9        | 1215   | 9     | AY407058 Homo sapi |
| 6          | 921.6  | 40.4        | 1063   | 1     | AL548548 AL548548  |
| 7          | 918.8  | 40.3        | 1028   | 1     | AL573084 AL573084  |
| 8          | 840.6  | 36.8        | 960    | 5     | EX348832 BX348832  |
| 9          | 834    | 36.5        | 932    | 5     | EX391728 BX391728  |
| 10         | 798.8  | 35.0        | 1213   | 9     | AY407059 Pan trogl |
| 11         | 675.8  | 29.6        | 721    | 6     | CB528341 UI-H-F12- |
| 12         | 663.4  | 29.1        | 735    | 1     | AI862415 tdl6b10.x |
| 13         | 652.8  | 28.6        | 696    | 4     | BG714406 602669930 |
| 14         | 626    | 27.4        | 1218   | 9     | AY407060 Mus muscu |
| 15         | 611.8  | 26.8        | 647    | 1     | AI809922 wf59g08.x |
| 16         | 608.8  | 26.7        | 634    | 5     | BP307288 BP307288  |
| 17         | 595.4  | 26.1        | 787    | 4     | BG212051 RST31514  |
| 18         | 592.2  | 26.0        | 597    | 7     | CK903582 ie60e09.y |
| 19         | 584.4  | 25.6        | 598    | 5     | BP234525 BP234525  |
| 20         | 578    | 25.3        | 582    | 5     | BP347750 BP347750  |
| 21         | 576    | 25.2        | 650    | 7     | CF529257 UI-1-BC1p |
| 22         | 575.4  | 25.2        | 582    | 5     | BP321307 BP321307  |
| 23         | 575.4  | 25.2        | 593    | 5     | BX471613 DKFZp686H |
| 24         | 574.8  | 25.2        | 582    | 5     | BP320364 BP320364  |

|    |       |      |      |   |          |
|----|-------|------|------|---|----------|
| 25 | 573.4 | 25.1 | 579  | 5 | BP346252 |
| 26 | 562.6 | 24.7 | 756  | 1 | AI972163 |
| 27 | 556.2 | 24.4 | 561  | 4 | BI962885 |
| 28 | 550.4 | 24.1 | 590  | 2 | AW813491 |
| 29 | 546.2 | 23.9 | 551  | 4 | BI962932 |
| 30 | 538.4 | 23.6 | 714  | 4 | BG214591 |
| 31 | 537.2 | 23.5 | 4257 | 3 | AK088439 |
| 32 | 534.8 | 23.4 | 572  | 2 | BF062790 |
| 33 | 530.8 | 23.3 | 550  | 5 | BQ004033 |
| 34 | 530.4 | 23.2 | 582  | 6 | CB047127 |
| 35 | 503.4 | 22.1 | 834  | 7 | CO735207 |
| 36 | 489   | 21.4 | 921  | 6 | CB203297 |
| 37 | 479.2 | 21.0 | 819  | 7 | CO739225 |
| 38 | 478   | 20.9 | 743  | 4 | BI110230 |
| 39 | 475.4 | 20.8 | 517  | 7 | CR557075 |
| 40 | 475   | 20.8 | 804  | 7 | CO739081 |
| 41 | 470.4 | 20.6 | 512  | 5 | BX504641 |
| 42 | 463.4 | 20.3 | 510  | 5 | BX478886 |
| 43 | 456.8 | 20.0 | 510  | 1 | AA626077 |
| 44 | 449.4 | 19.7 | 487  | 2 | BF760470 |
| 45 | 448.4 | 19.6 | 592  | 5 | BP320006 |

## ALIGNMENTS

RESULT 1  
LOCUS CR620685  
DEFINITION full-length cDNA clone CS0DI037VG20 of Placenta Cot 25-normalized of Homo sapiens (human).  
ACCESSION CR620685  
VERSION CR620685.1 GI:50501492  
KEYWORDS HTC; CDSLT CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2134)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : feng liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ invitrogen Corporation 1600 Faraday Avenue  
REFERENCE 2 (bases 1 to 2134)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
COMMENT - Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
FEATURES  
source  
1. .2134  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DI037VG20"  
/tissue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

ORIGIN  
Query Match 92.7%; Score 2114.6; DB 3; Length 2134;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2130; Conservative 0; Mismatches 4; Indels 3; Gaps 1;  
Qy 65 GGGAGAGGAGCAAGGACCGTGAAGCTGCTGTGTAAGCTGACACAGCCCTCCAA 124  
|||||  
Db 1 GGGAGAGGAGCAAGGACCGTGAAGCTGCTGTGTAAGCTGACACAGCCCTCCAA 60

|    |      |   |      |
|----|------|---|------|
| QY | 125  | GTGAGCAGCACTGTTCTTCTCCCACTGCAATCTGACAGTTTCTGATGCTCGGAGAGAA      | 184  |
| Db | 61   | GTGAGCAGCACTGTTCTTCCCACTGCAATCTGACAGTTTCTGATGCTCGGAGAGAA        | 120  |
| QY | 185  | CAGCAGTAAACACAGGTTTGCTACTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG        | 244  |
| Db | 121  | CAGCAGTAAACACAGGTTTGCTACTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG        | 180  |
| QY | 245  | ACCCAGCCATGCGAGCGTAGCAGCCTGCTGTTTTCAGACGCGCAGCAGCTCGGAGCTCTGGA  | 304  |
| Db | 181  | ACCCAGCCATGCGAGCGTAGCAGCCTGCTGTTTTCAGACGCGCAGCAGCTCGGAGCTCTGGA  | 240  |
| QY | 305  | CGTGTGTTTCCCTCAAGTTTGCCTAAGCTGCTGGTTTATTTACTGAGAGAAAGAGAGAGAG   | 364  |
| Db | 241  | CGTGTGTTTCCCTCAAGTTTGCCTAAGCTGCTGGTTTATTTACTGAGAGAAAGAGAGAGAG   | 300  |
| QY | 365  | GAATGTTTCTTTTACTCTGAGCTGTGATCTTGTCTTGGCGGAGCGCTATAACAACTTTTCG   | 424  |
| Db | 301  | GAATGTTTCTTTTACTCTGAGCTGTGATCTTGTCTTGGCGGAGCGCTATAACAACTTTTCG   | 360  |
| QY | 425  | GAAGAGATGGACAGCATAGGAAGAGCAATATCAGGTCCAGCATGGGTCTCTGAGCTTA      | 484  |
| Db | 361  | GAAGAGATGGACAGCATAGGAAGAGCAATATCAGGTCCAGCATGGGTCTCTGAGCTTA      | 420  |
| QY | 485  | CACCTTCTCTCCAGAGATGGAACAACTGCGGCTCTTCTCCAGCCCCCTACGTGTCCAA      | 544  |
| Db | 421  | CACCTTCTCTCCAGAGATGGAACAACTGCGGCTCTTCTCCAGCCCCCTACGTGTCCAA      | 480  |
| QY | 545  | TGCTGTGACAGGAGCGCGCGCTGGAATACGATGACTCGGTGCGAGAGCTGCAAGTGTCT     | 604  |
| Db | 481  | TGCTGTGACAGGAGCGCGCGCTGGAATACGATGACTCGGTGCGAGAGCTGCAAGTGTCT     | 540  |
| QY | 605  | GGAGAACATCATGGGAAAACAACTCAGTGGCTTAATGAACTTGAAGATTTATATCCAGGA    | 664  |
| Db | 541  | GGAGAACATCATGGGAAAACAACTCAGTGGCTTAATGAACTTGAAGATTTATCCAGGA      | 600  |
| QY | 665  | CAACATGAAAGAGAAATGGTAGATACAGAGAAATGCAATGACAGAACCCAGACCGGCTGT    | 724  |
| Db | 601  | CAACATGAAAGAGAAATGGTAGATACAGAGAAATGCAATGACAGAACCCAGACCGGCTGT    | 660  |
| QY | 725  | GATGATAGAAATAGGAGCAAACTGTTGAAACAAACAGCTGAGGCAAAACCGGAAAGTTAAC   | 784  |
| Db | 661  | GATGATAGAAATAGGAGCAAACTGTTGAAACAAACAGCTGAGGCAAAACCGGAAAGTTAAC   | 720  |
| QY | 785  | TGATGTGGAAGCCCAAGTATTAATCAGACCCAGAGACTTGAATCTCAGCTCTTGAAACA     | 844  |
| Db | 721  | TGATGTGGAAGCCCAAGTATTAATCAGACCCAGAGACTTGAATCTCAGCTCTTGAAACA     | 780  |
| QY | 845  | CTCCCTCTCGACAAACAAATTTGAAAAACAGATTTTGGACCCAGACAGTGAATTAACAA     | 904  |
| Db | 781  | CTCCCTCTCGACAAACAAATTTGAAAAACAGATTTTGGACCCAGACAGTGAATTAACAA     | 840  |
| QY | 905  | ATTGCAAGATAGACAGTTTCTAGAAAGAGGTGTAGCTATGGAAGACAGACAT            | 964  |
| Db | 841  | ATTGCAAGATAGACAGTTTCTAGAAAGAGGTGTAGCTATGGAAGACAGACAT            | 900  |
| QY | 965  | CATCCAACTACAGTCAATTAAGAGAGAGAGATCAGCTACAGGTGTAGTATCAAGCA        | 1024 |
| Db | 901  | CATCCAACTACAGTCAATTAAGAGAGAGAGATCAGCTACAGGTGTAGTATCAAGCA        | 960  |
| QY | 1025 | AAATTCATCATGTAAGAACTAGAAAAAATAATAGTGAATGCAATGCAAGTGAATTAATTCAGT | 1084 |
| Db | 961  | AAATTCATCATGTAAGAACTAGAAAAAATAATAGTGAATGCAATGCAAGTGAATTAATTCAGT | 1020 |
| QY | 1085 | TCTTCAAGAGAGCAACATGATCTCATGAGACAGTTAATTAATCTTACAGCTATGATGTC     | 1144 |
| Db | 1021 | TCTTCAAGAGAGCAACATGATCTCATGAGACAGTTAATTAATCTTACAGCTATGATGTC     | 1080 |
| QY | 1145 | CACATCAAACTCAGCTAAGGACCCCACTGCTGCTAAAGAGAGCAAACTCAGCTTCAGAGA    | 1204 |
| Db | 1081 | CACATCAAACT---CTAAGACCCCACTGCTGCTTAAGAGAGCAAACTCAGCTTCAGAGA     | 1137 |

RESULT 2

BC022490

LOCUS

DEFINITION

Homo sapiens cDNA clone IMAGE:4792831, containing frame-shift

2083 bp mRNA

linear

HTC 12-OCT-2004



|                            |  |
|----------------------------|--|
| errors.                    |  |
| ACCESSION                  | BC022490   |
| VERSION                    | BC022490.1   |
| KEYWORDS                   | GI:18490680  |
| SOURCE                     | HTC.   |
| ORGANISM                   | Homo sapiens (human)   |
| REFERENCE                  | Homo sapiens   |
| AUTHORS                    | 1 (bases 1 to 2083)<br>Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toohiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. |
| TITLE                      | Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences   |
| JOURNAL                    | Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  |
| PUBLISHED                  | 12477932   |
| REFERENCE                  | 2 (bases 1 to 2083)  |
| AUTHORS                    | Director MGC Project.  |
| TITLE                      | Direct Submission  |
| JOURNAL                    | Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA   |
| REMARK                     | NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>   |
| COMMENT                    | Contact: MGC help desk<br>Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a><br>Tissue Procurement: Niklos Palkovits, M.D., Ph.D.<br>cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)<br>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)<br>DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305<br>Web site: <a href="http://www.shgc.stanford.edu">http://www.shgc.stanford.edu</a><br>Contact: (Dickson, Mark) <a href="mailto:mcd@paxil.stanford.edu">mcd@paxil.stanford.edu</a><br>Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.   |
| FEATURES                   | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a><br>Series: IRAC Plate: 32 Row: b Column: 11<br>This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557314<br>This clone has the following problem: frame shifted.<br>Location/Qualifiers<br>1..2083<br>/organism="Homo sapiens"<br>/mol_type="mRNA"<br>/db_xref="taxon:9606"<br>/clone="IMAGE:4792831"<br>/tissue_type="Brain, hypothalamus"<br>/clone_lib="NIH MGC_96"<br>/lab_host="DH10B"<br>/note="vector: pBluescript"   |
| source                     |  |
| ORIGIN                     |  |
| Query Match                | 88.9%; Score 2029.2; DB 3; Length 2083;  |
| Best Local Similarity      | 99.4%; Pred. NO. 0;  |
| Matches 2058; Conservative | 0; Mismatches 8; Indels 4; Gaps 2;   |
| 162                        | TTACTGATGCTCTGGAGAGAAACACAGCATTAATAAACACAGGTTTGCTACTGCTGAAAAGAGG 221   |
| 3                          | TTACTGATGCTCTGGAGAGAAACACAGCATTAATAAACACAGGTTTGCTACTGCTGAAAAGAGG 62  |
| 222                        | AAAGAGAAGACTTTTCAATTCAGCGACCCAGCCATGGCAGCGTAGCAGCCCTCGGTTTCAGA 281   |
| 63                         | AAAGAGAAGACTTTTCAATTCAGCGACCCAGCCATGGCAGCGTAGCAGCCCTCGGTTTCAGA 122   |
| 282                        | CGGACAGCAGCTCGGGACTCTCGGACGTGTGTGTCCTCAAGTTTGTGAAGCTGCTGCTTT 341   |
| 123                        | CGGACAGCAGCTCGGGACTCTCGGACGTGTGTGTCCTCAAGTTTGTGAAGCTGCTGCTTT 182   |
| 342                        | ATTACTGAAGAAAGATGTGGCAGATTTGTTTCTTACTCTGAGCTGTGATCTTGCTTG 401  |
| 183                        | ATTACTGAAGAAAGATGTGGCAGATTTGTTTCTTACTCTGAGCTGTGATCTTGCTTG 242  |
| 402                        | GCCGACGCTTATTAACACTTTCCGAGAGCATGACGACATAGGAAGAGCAATATATCAG 461   |
| 243                        | GCCGACGCTTATTAACACTTTCCGAGAGCATGACGACATAGGAAGAGCAATATATCAG 302   |
| 462                        | GTCCAGCATGGGTCTCTGACGTACACTTCTCTGCGAGATGGAACAATGCGCTCT 521   |
| 303                        | GTCCAGCATGGGTCTCTGACGTACACTTCTCTGCGAGATGGAACAATGCGCTCT 362   |
| 522                        | TCCTCAGACCCCTACGTTGTCATGTCGTGAGAGGACGCGCGCTCGAATACGATGAC 581   |
| 363                        | TCCTCAGACCCCTACGTTGTCATGTCGTGAGAGGACGCGCGCTCGAATACGATGAC 422   |
| 582                        | TCGGTCGAGGCTGCAAGTCTGGAGAACATCATGGAACCAACACTCAGTGGCTAATG 641   |
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| 642                        | AAGCTTGAGATTTATATCCAGGACCAACATCAAGAAAGAAATGGTAGATACAGCAGAT 701   |
| 483                        | AAGCTTGAGATTTATATCCAGGACCAACATCAAGAAAGAAATGGTAGATACAGCAGAT 542   |
| 702                        | GCAGTACAGAACCCAGCGCTGTGATGATAGAAATAGGGAACAACCTGTTGAACCAACA 761   |
| 543                        | GCAGTACAGAACCCAGCGCTGTGATGATAGAAATAGGGAACAACCTGTTGAACCAACA 602   |
| 762                        | GCTGAGCAACCGGAGTTAACTGATGTCGAGGCCCAAGTNTAATTAAGAGCAAGATCAG 821   |
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| 822                        | CTTGAAGCTTCAGCTCTTGGAACTCTCCCTCTCGACAAACAAATTTGGAACCAAGATTTG 881   |
| 663                        | CTTGAAGCTTCAGCTCTTGGAACTCTCCCTCTCGACAAACAAATTTGGAACCAAGATTTG 722   |
| 882                        | GACCAGACCAAGTGAATAAACAATTTGCAAGATAAGAACAGTTTCTTAGAAAGAGGTG 941   |
| 723                        | GACCAGACCAAGTGAATAAACAATTTGCAAGATAAGAACAGTTTCTTAGAAAGAGGTG 782   |
| 942                        | CTAGCTATGAAGCAAGCAATCATCTCACTACAGTCAATTAAGAGCAAGATCAG 1001   |
| 783                        | CTAGCTATGAAGCAAGCAATCATCTCACTACAGTCAATTAAGAGCAAGATCAG 842  |
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| 843                        | CTACAGGTGTTAGTATCCAAAGCAAAATTTCCATCATTTGAGAACTAGAAAAAATAGTG 902  |
| 1062                       | ACTGCCACCGGTGAATAATTCAGTTTCTCAAGCAGCAACATGATCTCATGGACAGTT 1121   |
| 903                        | ACTGCCACCGGTGAATAATTCAGTTTCTCAAGCAGCAACATGATCTCATGGACAGTT 962  |
| 1122                       | AATTAAGTACTGATGATGTCAGATCAATCACTAGCTAAGGACCCCTGTTGCTAAA 1181   |
| 963                        | AATTAAGTACTGATGATGTCAGATCAATCACTAGCTAAGGACCCCTGTTGCTAAA 1019   |
| 1182                       | GAAGAACAAATCAGCTTTGAGAGCTGTGCTGAAGTATTCAATCAGGACACACCAAAAT 1241  |
| 1020                       | GAAGAACAAATCAGCTTTGAGAGCTGTGCTGAAGTATTCAATCAGGACACACCAAAAT 1079  |

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| 1242 | QY | GGCATCTACAGCTTAA          | CATTCCCTTAATTTCTACAGAGAGATCAAGGCTTACTGTGACATG | 1301 |
| 1080 | Db | GGCATCTACACGTTTAA         | CATTCCCTTAATTTCTACAGAGAGATCAAGGCTTACTGTGACATG | 1139 |
| 1302 | QY | GAAGCTGGAGGAGCGGCTGGA     | CAATTTATTTTCAGCGAGCTGAGGATGCACGCTTGATTGTTTT   | 1361 |
| 1140 | Db | GAAGCTGGAGGAGCGGCTGGA     | CAATTTATTTTCAGCGAGCTGAGGATGCACGCTTGATTGTTTT   | 1199 |
| 1362 | QY | CAGAGGACTTTGGAAAGAATA     | TAAAGTGGGATTTTGGTAAACCTTTTCAGGAGAAATATGGCTG   | 1421 |
| 1200 | Db | CAGAGGACTTTGGAAAGAATA     | TAAAGTGGGATTTTGGTAAACCTTTTCAGGAGAAATATGGCTG   | 1259 |
| 1422 | QY | GGAAATGAGTTTGTTCGCAACT    | GACTAATTCAGGCAACGCTATGTGCTTAAAAATACACCTT      | 1481 |
| 1260 | Db | GGAAATGAGTTTGTTCGCAACT    | GACTAATTCAGGCAACGCTATGTGCTTAAAAATACACCTT      | 1319 |
| 1482 | QY | AAAGACTGGGAAGGGGAATGAGGCT | TACTCATTTGTATGAACAATTTCTATCTCTCAAGTGAA        | 1541 |
| 1320 | Db | AAAGACTGGGAAGGGGAATGAGGCT | TACTCATTTGTATGAACAATTTCTATCTCTCAAGTGAA        | 1379 |
| 1542 | QY | GAACTCAATTTATAGGATTCACCT  | TAAAGGACTTACAGGGAACGCCGCAAAATAAGCAGC          | 1601 |
| 1380 | Db | GAACTCAATTTATAGGATTCACCT  | TAAAGGACTTACAGGGAACGCCGCAAAATAAGCAGC          | 1439 |
| 1602 | QY | ATCAGCCCAACCGGAATGATTTTAG | CACAAAGGATGGAGCAACGCAAAATGATTTGCT             | 1661 |
| 1440 | Db | ATCAGCCCAACCGGAATGATTTTAG | CACAAAGGATGGAGCAACGCAAAATGATTTGCT             | 1499 |
| 1662 | QY | AAATGTTTCACAAATGCTTAACAGG | AGGCTGGTGGTTTGATGCATGTGCTCTCCAACTTG           | 1721 |
| 1500 | Db | AAATGTTTCACAAATGCTTAACAGG | AGGCTGGTGGTTTGATGCATGTGCTCTCCAACTTG           | 1559 |
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| 1781 | QY | CTACTGGAAGGCTCAGGCTATTGCT | CAAGGCCACCAACCATGATGATCCGACCAGCAGA            | 1840 |
| 1620 | Db | CTACTGGAAGGCTCAGGCTATTGCT | CAAGGCCACCAACCATGATGATCCGACCAGCAGA            | 1679 |
| 1841 | QY | TTTCTAAACATCCAGTCCACCTGAG | GAACTGTCTCGAACTATTTTCAAAAGACTTAAAGCC          | 1900 |
| 1680 | Db | TTTCTAAACATCCAGTCCACCTGAG | GAACTGTCTCGAACTATTTTCAAAAGACTTAAAGCC          | 1739 |
| 1901 | QY | CAGTGCATGAAAGTCAAGGCTGGC  | ACTGTGTCTCTTCCACACAGAGGGCGTGTGCT              | 1960 |
| 1740 | Db | CAGTGCATGAAAGTCAAGGCTGGC  | ACTGTGTCTCTTCCACACAGAGGGCGTGTGCT              | 1799 |
| 1961 | QY | CGGTGCTGACGGGACCCACATGCT  | CACAGATTAGAGCCTGTAAACTTTATCACTTAAACTT         | 2020 |
| 1800 | Db | CGGTGCTGACGGGACCCACATGCT  | CACAGATTAGAGCCTGTAAACTTTATCACTTAAACTT         | 1859 |
| 2021 | QY | GCATCACTTAAACCGAACCAAGAC  | AGCCCTAAACATCCATAATTTGTGATTAGACAGAAACA        | 2080 |
| 1860 | Db | GCATCACTTAAACCGAACCAAGAC  | AGCCCTAAACATCCATAATTTGTGATTAGACAGAAACA        | 1919 |
| 2081 | QY | CCTATGCAAAAGATGAACCCGAGG  | CTGAGATCAGACTGACAGTTTACAGACGCTGCTGTC          | 2140 |
| 1920 | Db | CCTATGCAAAAGATGAACCCGAGG  | CTGAGATCAGACTGACAGTTTACAGACGCTGCTGTC          | 1979 |
| 2141 | QY | ACAACCAAGAAATGTTATGTGCA   | AGTTTATCAGTAAATAACTGGAAAAACAGAACTTATG         | 2200 |
| 1980 | Db | ACAACCAAGAAATGTTATGTGCA   | AGTTTATCAGTAAATAACTGGAAAAACAGAACTTATG         | 2039 |
| 2201 | QY | TTATACAATAACAGATCATCTTTG  | GAACCTGCA 2230                                |      |
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|------------|---|---------|------|--------|-----------------|--|
| RESULT 3   |   |         |      |        |                 |  |
| AK048622   |   |         |      |        |                 |  |
| LOCUS      | AK048622  | 2443 bp | mRNA | linear | HTC 03-APR-2004 |  |
| DEFINITION | Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library clone |         |      |        |                 |  |

library, clone: C130089A05 product: ANGIOPOIETIN-2 PRECURSOR, full insert sequence.  
AK048622  
VERSION AK048622.1 GI:26339449  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
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PUBMED 10349636  
2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
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3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Iehii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
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20530913  
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4  
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5  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
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Nature 420, 563-573 (2002)  
6 (pages 1 to 2443)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
TITLE  
JOURNAL  
COMMENT

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>

URL: <http://fantom.gsc.riken.jp/>

#### FEATURES

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polya\_site

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#### ORIGIN

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| Qy | 113 | CAGCCCTCCCAAGTGAGGAGGACGTCTTCCCACTGCAATCTGACAGTTTACTGCGATGC    | 172 |
| Db | 12  | CAGACCTCTGGAGTGAGCGGGCTGCTCTCTCTCAGGACAGCTCCGAGTGTCGGGG        | 71  |
| Qy | 173 | CTGGAGAGACACAGCAGTAAACCAGGTTTGCTACTGGAAAAGAGAGAAAGAGAC         | 232 |
| Db | 72  | GAGAAGAGAGAGAGAGACAGGCACCTGGGAAAGAGCCTG--CTGCGGACGGAGAGGC      | 129 |
| Qy | 233 | TTTCATTTGACGGACCCAGCCATGGCAGCGTAGCAGCCCTGCGTTTTCAGACGGCAGCAGCT | 292 |
| Db | 130 | TCTCACTGATGACTATTCA---CAGCGCACAGCCCTGTGCCTTAGA---CAGCAGCT      | 182 |
| Qy | 293 | CGGACCTCTGGAAGCTGTTTGGCCCTCAAGTTTGGTGAAGCTGCTGCTTATTCTGAGA     | 352 |
| Db | 183 | GAGAGCTCAGACCGCAAGTTTGC-----TGAACCTCAGAGTTTAGAACCCAAAAAGAGAGA  | 237 |
| Qy | 353 | AAGAATGTCAGATGTTTCTTCTTACTCTCAGCTGTGATCTCTCTGTGGCGCAGCCTA      | 412 |
| Db | 238 | GAGAATGTGGCAGATCATTTTCTTAACCTTTTGGCTGGGATCTTGTCTTGGCCTCAGCCTA  | 297 |
| Qy | 413 | TAAACAATTTTCGGAAGAGCATGGACAGCATAGGAAAGAGCAATATCAGGTCCAGCATGG   | 472 |
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| Qy | 473 | GTCTGCACTACACTTTTCTCTCCGACAGAGATGGACAACTGCGGCTTCTCTCCAGCCC     | 532 |
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| Db | 418 | CTACATGTCCAATGCCGTGCAAGGGATGCAACCCCTCGACTACGACGAGTCAAGTGA      | 477 |

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|----|------|--|------|
| Qy | 593  | GCTCAAGTGTGGAGAACATCATGTGAAACCAACACTCAGTGGCTAATGAAGCTTGAGAA      | 652  |
| Db | 478  | GCTGCAAGTGTGGAGAACATCTTAGAGAACCAACACACAGTGGCTATGAAGCTGGAGAA      | 537  |
| Qy | 653  | TTATATCCAGGACCAACATGAAGAAAGAAATGGTAGAGATACAGCAGAAATCAGCTACAGAA   | 712  |
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| Qy | 713  | CCAGAGCGCTGTGATGATAGAAATAGGGAACAACTCTGTTGAAACCAACACAGCTGAGCAAAAC | 772  |
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| Db | 658  | TCGGAATCTGACTGATGTGAAGCCCAAGTACTAAACCAAGCAGCAGAGCTTCAGCTGCA      | 717  |
| Qy | 833  | GCTCTTTGGAACACTCCCTCTCTCGAACAAATTTGGAATAAAGAGATTTTGGACCAAGACAG   | 892  |
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| Qy | 1253 | GTTAAACATTCCTTAATTTTACAGAGAGATCAAGGCCCTACTGTGACATGGAAGCTGAGG     | 1312 |
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| Qy | 1313 | AGCGGGTGGACAAATTTATTCAGCGAGCTGAGGATGGCAGCGTTGATTTTTCAGAGGACGTG   | 1372 |
| Db | 1198 | AGGAGGGTGGACAGTCTATCCAAACCGAGAGAGATGGCAGTGTGGACTTCCAGAGGACGTG    | 1257 |
| Qy | 1373 | GAAAGAAATATAAGTGGGATTTGGTAAACCTTCAGGAGAAATATTGGCTGGGAAATGAGTT    | 1432 |
| Db | 1258 | GAAAGAAATACAAAGAGGGCTTCGGAGCCCTCTGGGAGAGTACTGGCTGGGCATGAGTT      | 1317 |
| Qy | 1433 | TGTTTCGCAACTGACTAATCAGCAACCGCTATGTGCTTTAAATAACACCTTTAAAGACTGGGA  | 1492 |
| Db | 1318 | TGCTCCAGCTGACCGGTGAGCACCGCTACGCTGCTTAAAGATCCAGCTGGAAGGACTGGGA    | 1377 |
| Qy | 1493 | AGGAAATGAGGCTTACTCATTTGATGAAATTTCTATCTCTCAAGTGAAGACTCAATTA       | 1552 |
| Db | 1378 | AGGCACAGCGCGCATTCGCTGTATGATCACTTCTACTCTGCTGGTGAAGAGTCCAACTA      | 1437 |
| Qy | 1553 | TAGGATTCACCTTAAAGGACTTACAGGGACAGCGCGCAAAATAAGCAGCAGCATCAGCCAAAC  | 1612 |
| Db | 1438 | CAGATTCACCTTACAGGACTTACCGGGACCGCGGGCAAAATAAGTAGCATCAGCCCAAC      | 1497 |
| Qy | 1613 | AGGAAATGATTTTAGCAACAAAGGATGGAGACAAACGACAAATATGTTTTCGAAATTTTCCACA | 1672 |
| Db | 1498 | AGGAAATGATTTTAGCACAAAGGATTCGGCAATGACAAATGCATCTGCAAGTGTGCCA       | 1557 |
| Qy | 1673 | AATGCTAACAGGAGGCTGGTGGTTTGTGATGCAATGTGGTCTCTTCCAACTTGAACGGAATGA  | 1732 |



|   |   |    |      |   |      |
|---|---|----|------|---|------|
| CDS   | 274..1764   | Db | 690  | TCGGAACCTGACTGATGTGGAAGCCCAAGTACTAATACACAGACCAAGACTCGAGCTGCA      | 749  |
| /note="unnamed protein product; ANGIOPOIETIN-2 PRECURSOR (SWISSPROT 035608, evidence: FASTY, 99.6%ID, 100%length, match=1488) putative" | /codon_start=1<br>/protein_id="BAB31887.1"<br>/db_xref="GI:12860232"<br>/translation="MMQIIPLTFGMDLVLASVSNFRKVDSTGRRQYQVQNGPCSYT<br>FLLPEDSRSSSPVMSNAVORDADLDYDDSVORLQVLENNLENNLWMLKLENIYQ<br>DNMKEMVEIQNVQVONQAVMLEIGTSLNLTAAOTRKLTDVAAVLNLTORLEIQL<br>LQHSITNKLKQILQDTSINKLQNKSNFLEOKVLDNKGKSEQLQSMKEQKDLQV<br>LVQKQSVDELEKLLVATVNSLQKQKQHDLMETVNSLLTMSFNSPNSKSVLRKE<br>EQTTPRDCAEIKFSKGTISGITYLTFPNSFTTEIKAYCDMDVGGGVTWVOHREDGSDV<br>FORTWKEYGFGSGEYWLGNFVSLQTHQRYVLKIQLDWEGNEHARSYDHPYL<br>AGPESNRYHLTGLTGTAGKISSISQPSGDFSTKDSNDKCIKCSQMLSGGWFPDAG<br>GPNLNGQYYPQKQNTNKNGIKWYWKSGSYSLKATTWIRPADP" | Qy | 833  | GCTCTGGGAACACTCCCTCTCGACAAAACAAATTTGGAATAACAGATTTTGGACCAAGACCAG   | 892  |
|   |   |    | 750  | GCTTCTCCAAACATCTTATTTCTACCAACAAATTTGGAATAACAGATTTTGGATCAGACCCAG   | 809  |
|   |   |    | 893  | TGAAATATAACAAATTTGCAAGATAAGAACAGTTTCTTAGAAAAGAGAGTGTCTAGCTATGGA   | 952  |
| /note="putative"  | /polyA_signal<br>/polyA_site  | Db | 810  | TGAATATAACAAAGCTACAAATAAGAACAGCTTCTTAGAACAGAAAGTTCTTGACATGGA      | 869  |
|   |   |    | 953  | AGACAAGCACATCATCCAACTACAGTCAATATAAAGAGAGAAAGATCAGCTACAGGTGTT      | 1012 |
|   |   |    | 870  | GGCAAGCACAGCGAGCAGCTACAGTCCATGAAGAGAGAGAGGACGAGCTCCAGGTGCT        | 929  |
| /note="putative"  | /polyA_signal<br>/polyA_site  | Qy | 1013 | AGTATCCAAAGCAAAATTTCCATCATTAAGAACTAAGAAAATAATAGTGTGCTCCAGGT       | 1072 |
|   |   |    | 930  | GGTGTCCAAAGCAGAGCTCTGTCTATTCAGCAGCTGGAGAAAGCTGGTGAACGCCACGGT      | 989  |
|   |   |    | 1073 | GAATATTCAGTTCTTCAAAAGCAGCAACATGATCTCATGGAGACAGTAAATTAATTTACT      | 1132 |
| /note="putative"  | /polyA_signal<br>/polyA_site  | Db | 990  | CAACAACTCGCTCTTTCAGAGCAGCAGCATGACCTAATGGAGACCGTCAACAGCTTGCT       | 1049 |
|   |   |    | 1133 | GACTATGATGTCCACATCAAACTCAGCTAAGGACCCCACTGTTTGTAAAGAAGAACAAAT      | 1192 |
|   |   |    | 1050 | GACCATGATGTATCAACCCCACTCCAAAGAGCTCGGTGCTATCCGTAAAGAAGCAAAAC       | 1109 |
| /note="putative"  | /polyA_signal<br>/polyA_site  | Qy | 1193 | CAGCTTCAGAGACTGTGTGAAGTATTCAAATCAGACACACACAAATGGCATCTACAC         | 1252 |
|   |   |    | 1110 | CACCTTCAGAGACTGTGTGCGAAATCTTCAAGTCAGGACTCACCAACAGTGGCATCTACAC     | 1169 |
|   |   |    | 1253 | GTTAACTTCCCTAATTTCTACAGAGAGATCAAGGCTTCAAGTGTGATGACATGGAAGCTGGAGG  | 1312 |
| /note="putative"  | /polyA_signal<br>/polyA_site  | Db | 1170 | ACTGACCTTCCCACTCCACAGAGAGATCAAGGCTTCAAGTGTGATGACATGGAAGCTGGAGG    | 1229 |
|   |   |    | 1313 | AGCGGCTGACAAATTTATTCAGCGAGCTGAGAGTGGCAGGCTTGAATTTTCAGAGGACTTG     | 1372 |
|   |   |    | 1230 | AGAGGGTGGACAGTCAATCCACACCGAGAGAGATGGCAGTGTGGACTTCCAGAGGACGTG      | 1289 |
| /note="putative"  | /polyA_signal<br>/polyA_site  | Qy | 1373 | GAAAGAAATATAAGTGGGATTTGGTAAACCTTCAGGAGAAATATTTGGCTGGGAAATGAGTT    | 1432 |
|   |   |    | 1290 | GAAAGAAATACAAAGAGGGCTTCGGGAGCCCTCTGGGAGAGTACTGGCTGGCAATGAGTT      | 1349 |
|   |   |    | 1433 | TGTTTGGCAACTGACTAATCAGCAACGCTATGTCTTAAATACACCTTAAAGACTCGGA        | 1492 |
| /note="putative"  | /polyA_signal<br>/polyA_site  | Db | 1350 | TGTCTCCAGCTGACCGGTCAGCACCGCTACGCTTAAGATCCAGCTGAAGGACTGGGA         | 1409 |
|   |   |    | 1493 | AGGGAATGAGGCTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTA      | 1552 |
|   |   |    | 1410 | AGGCAAGAGGCGCATTCGCTGTATGATCACTTCTCTCTCGCTGGTGAAGTCCAACTA         | 1469 |
| /note="putative"  | /polyA_signal<br>/polyA_site  | Qy | 1553 | TAGGATTCACCTTAAAGGACTTACAGGACAGCGCGCAAAATTAAGCAGATTCAGCCAAAC      | 1612 |
|   |   |    | 1470 | CAGGATTCACCTTACAGGACTCAGCGGACCGCGGCAAAATAAGTAGCATTCAGCCAAAC       | 1529 |
|   |   |    | 1613 | AGGAATGATTTAGCAAAAGGATGGAGACAACGACAAATGATTTTGGCAATGTTCCACA        | 1672 |
| /note="putative"  | /polyA_signal<br>/polyA_site  | Db | 1530 | AGGAATGATTTAGCAAAAGGATTTCCGACAAATGACAAATGTCATCTGCAAGTGTGCCA       | 1589 |
|   |   |    | 1673 | AATGCTAAACAGGAGGCTGGTGGTTTGTATGATGTGGTCTTCCAACTTGAACCGGAATGTA     | 1732 |
|   |   |    | 1590 | GATGCTCTCAGGAGGCTGGTGGTTTGGCAATGTTGCTTCCAACTTGAATGACAGTA          | 1649 |
| /note="putative"  | /polyA_signal<br>/polyA_site  | Qy | 1733 | CTATCCACAGAGGCGAGAACAAATTAAGTTCAAGCGCATTAATTTGGTACTACTCGAAAGG     | 1792 |
|   |   |    | 1650 | CTACCCCAAAAACAGAAATACAAATTAAGTTTAAAGGATCAAGTGGTACTACTTGAAGGG      | 1709 |
|   |   |    | 1793 | CTCAGGCTATTTCGCTCAAGGCGCAACCATGATGATCCGACCGACAGATTTCTTAAACATC     | 1852 |
| /note="putative"  | /polyA_signal<br>/polyA_site  | Db | 1710 | GTCCGGCTACTCGCTCAAGGCGCAACCATGATGATCCGGCAGCAGATTTCTTAAATGCC       | 1769 |
|   |   |    | 1853 | CCAGTCCACTGAGGAATCTCTCGAACTATTTTCAAGACTTTTAAAGCCCACTGACCTGAA      | 1912 |
|   |   |    | 1770 | TGCCTACACTACCCAGAAAGAACTTGTCTGC-----ATCCAAAGATTAACTCCAAAGGCACTGAG | 1825 |







|  |      |   |                                     |
|--|------|---|-------------------------------------|
| Db   | 174  | ACGGACCAAGCAAGACCCCTAAACATCCATAATTGTGATTAGACAGAACACCTTATGCAA  | 115                                 |
| Qy   | 2090 | AGATGAACCCGAGGCTGAGAATCAGACTGACAGTTTACAGACGCTGCTGTCAACAACCAAG | 2149                                |
| Db   | 114  | AGATGAACCCGAGGCTGAGAATCAGACTGACAGTTTACAGACGCTGCTGTCAACAACCAAG | 55                                  |
| Qy   | 2150 | AATGTTATGTGCAAGTTTATCAGTAAA--TAACTGGAAAAACAGAACACTTATGT       | 2201                                |
| Db   | 54   | AATGTTATGTGCAAGTTTATCAGTAAA--TAACTGGAAAAACAGAACACTTATGT       | 1                                   |
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| BX348832   |      | 960 bp  | mRNA                                |
| LOCUS  |      |   |                                     |
| DEFINITION   |      |   |                                     |
| ACCESSION  |      |   |                                     |
| VERSION  |      |   |                                     |
| KEYWORDS   |      |   |                                     |
| SOURCE   |      |   |                                     |
| ORGANISM   |      |   |                                     |
| REFERENCE  |      |   |                                     |
| AUTHORS  |      |   |                                     |
| TITLE  |      |   |                                     |
| JOURNAL  |      |   |                                     |
| COMMENT  |      |   |                                     |
| Query Match  |      | 36.8%   | Score 840.6; DB 5; Length 960;      |
| Best Local Similarity  |      | 95.2%   | Pred. No. 1.5e-220;                 |
| Matches  | 916; | Conservative  | 0; Mismatches 38; Indels 8; Gaps 5; |
| Qy   | 844  | ACTCCCTCTCGACAAAACAAATTGGAAAAACAGATTGTCGACAGACAGTGAATAAACA    | 903                                 |
| Db   | 5    | ACACTCCCTCTCGACAAACAAATTGGAAAAAC-GAATTTGGACACAGACAGTGAATAAACA | 63                                  |
| Qy   | 904  | RATTGCAAGATAAGACAGTTTCTTACGAAGAAGAGTGTACGTATGAGACAGACACA      | 963                                 |
| Db   | 64   | AATTGCAAGATAAGACAGTTTCTTACGAAGAAGAGTGTACGTATGAGACAGACACA      | 123                                 |
| Qy   | 964  | TCATCCAACTACAGTCAATAAAGACAGAAAAAGATCAGCTACAGTGTAGTATCCAAGC    | 1023                                |
| Db   | 124  | TCATCCAACTACAGTCAATAAAGACAGAAAAAGATCAGCTACAGTGTAGTATCCAAGC    | 183                                 |
| Qy   | 1024 | AAATTTCCATCATTTGAAGAACTAGAAAAAATAATAGTGTCCACCGGTGAATTAATTCAG  | 1083                                |
| Db   | 184  | AAATTTCCATCATTTGAAGAACTAGAAAAAATAATAGTGTCCACCGGTGAATTAATTCAG  | 243                                 |
| FEATURES   |      |   |                                     |
| source   |      |   |                                     |
| Location/Qualifiers  |      |   |                                     |
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| /clone="CS0DI037YG20"  |      |   |                                     |
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| /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"   |      |   |                                     |
| /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4496.r |      |   |                                     |
| For more information about this cluster, see   |      |   |                                     |
| http://www.genoscope.cns.fr/cdna?s=CS0BAG030ZC09_CS02851_1&c=4496.r  |      |   |                                     |
| Qy   | 1190 | AATCAGCTTCAGAGCTGCTGGAAGTATTCAAATCAGACACACCAATGCGACTA         | 1249                                |
| Db   | 1009 | AATCTSTTCAGARACTGTGTAA--TWTTCAAATCGACWCACCAAGAT-CACTCA        | 953                                 |
| Qy   | 1250 | CAGTTAAACATTCCTTAATTCACAGAAGAGATCAAGGCCTACTGTGCATGGAAGCTGG    | 1309                                |
| Db   | 952  | CAGG-TWACATTCCTTAATTCACAGAAGAGATCAAGCCCTACTGTAACTGGAAGCTGG    | 894                                 |
| Qy   | 1310 | AGAGCGGGTGACAATTAATTCAGGACGTCGAGATGGCGGTGATTTTCAGAGAC         | 1369                                |
| Db   | 893  | AGGAGCGGGTGACAATTAATTCAGGACGTCGAGATGGCGGTGATTTTCAGAGAC        | 834                                 |
| Qy   | 1370 | TTGGAAGAATAAAGTGGGATTTGTAACCTTCAGGAGAAATATTCGCTGGGAATGA       | 1429                                |
| Db   | 833  | TTGGAAGAATAAAGTGGGATTTGTAACCTTCAGGAGAAATATTCGCTGGGAATGA       | 774                                 |
| Qy   | 1430 | GTTTGTTCGCAACTGACTAATCAGCAACGCTATGCTGTTAAATACACCTTAAAGACTG    | 1489                                |
| Db   | 773  | GTTTGTTCGCAACTGACTAATCAGCAACGCTATGCTGTTAAATACACCTTAAAGACTG    | 714                                 |
| Qy   | 1490 | GGAAGGAATGAGCTTACTCATTGTATGAACATTTCTCTCAAGTGAAGAACTCAA        | 1549                                |
| Db   | 713  | GGAAGGAATGAGCTTACTCATTGTATGAACATTTCTCTCAAGTGAAGAACTCAA        | 654                                 |
| Qy   | 1550 | TTATAGGATTCACCTTAAGGACTTACAGGACGCGCGGCAAAATAGCAGCATCAGCA      | 1609                                |
| Db   | 653  | TTATAGGATTCACCTTAAGGACTTACAGGACGCGCGGCAAAATAGCAGCATCAGCA      | 594                                 |
| Qy   | 1610 | ACCAGGAATGATTTTAGCAAAAGATGGAGACAAACACAAATGTATTTGCAATGCTC      | 1669                                |
| Db   | 593  | ACCAGGAATGATTTTAGCAAAAGATGGAGACAAACACAAATGTATTTGCAATGCTC      | 534                                 |
| Qy   | 1670 | ACAAATGCTAACAGGAGCTGCTGTTGATGATGCTGCTTCCAACTTGAACGGAAT        | 1729                                |
| Db   | 533  | ACAAATGCTAACAGGAGCTGCTGTTGATGATGCTGCTTCCAACTTGAACGGAAT        | 474                                 |
| Qy   | 1730 | GTACTATCCACAGAGCAGACAAATAAGTTCAACGGCATTAATGTTGTTACTACTGAA     | 1789                                |
| Db   | 473  | GTACTATCCACAGAGCAGACAAATAAGTTCAACGGCATTAATGTTGTTACTACTGAA     | 414                                 |
| Qy   | 1790 | AGGCTCAGGCTATTCGCTCAAGGCCACAAACATGATGTCGACAGCAGATTTCTAAAC     | 1849                                |
| Db   | 413  | AGGCTCAGGCTATTCGCTCAAGGCCACAAACATGATGTCGACAGCAGATTTCTAAAC     | 354                                 |
| Qy   | 1850 | ATCCAGTCCACTGAGGAACCTGCTCGAACTATTTTCAAGACTTAAGCCCGAGTCACT     | 1909                                |
| Db   | 353  | ATCCAGTCCACTGAGGAACCTGCTCGAACTATTTTCAAGACTTAAGCCCGAGTCACT     | 294                                 |
| Qy   | 1910 | GAAAGTCAGGCTGGCACTGTCTCTTCCACACAGAGGGCTGTCTCGTGTCTGA          | 1969                                |
| Db   | 293  | GAAAGTCAGG-TGGCGCACTGTCTCTTCCACACAGAGGGCTGTCTCGTGTCTGA        | 235                                 |
| Qy   | 1970 | CGGGACCCACATGCTCCAGATTAGAGCTGTAAACCTTTATCACTTTAACTTGCATCACTT  | 2029                                |
| Db   | 234  | CGGGACCCACATGCTCCAGATTAGAGCTGTAAACCTTTATCACTTTAACTTGCATCACTT  | 175                                 |
| Qy   | 2030 | AACGGACCAAGCAAGACCCCTAAACATCCATAATTGTGATTAGACAGAACACCTTATGCAA | 2089                                |

Email: seqrefgenoscope.cns.fr Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMWSPort 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
4496. r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?&CSDBAT021F06 CS01956 1&C=4496. r

**FEATURES**  
**source**

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Location/Qualifiers
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  /mol_type="mRNA"
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  /clone="CS001037YG20"
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  /clone_lib="Homo sapiens
  /note="1st strand cDNA w
  primer. Five prime end
  digested with Not I and
  sites of the pCMVSPORT 6

```

## ORIGIN

|                       |              |                     |       |             |
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| Query Match           | 36.5%;       | Score 834;          | DB 5; | Length 932; |
| Best Local Similarity | 96.7%;       | Prod. NO. 9,96-219; |       |             |
| Matches 004.          | Conservative | 0. Mismatches       | 23;   | Indels      |
|                       |              |                     | 8;    | Gaps        |
|                       |              |                     |       | 5;          |

|      |    |   |      |
|------|----|---|------|
| 453  | Qy | CAATATCAGGTCAGCATGGGTCTCGAGCTACATTTTCTCTCTCGCAGAGATGGACAAC      | 511  |
| 931  | Db |   | 872  |
|      |    | CAATATCAGGTCAGCATGGTCTCTCGAGCAAACTTTTCTCTTGGCAAAAGATGGACAAC     |      |
| 513  | Qy | TGCGGCT--CTTCTCTCAGCGCCCTACGTGTCCAATGCTGTGCAGAGGAAG-CGCGCGCTC   | 569  |
| 871  | Db |   | 812  |
|      |    | TGCGGCTTCTTCTNCCAGCCCTTAATTGTCCCATCTGTTCAGAAAGACGCGCGCGCTC      |      |
| 570  | Qy | G-AATACGATGACTCGGTGCAGAGGCTGCAGGTGCTGGAGAACTCATTGGAAAAACAAC     | 628  |
| 811  | Db |   | 752  |
|      |    | GAATACGATGACTCGGTGCAGAGGCTGCAAGTGTCTGNAGAACATCATTGGAAAAACAAC    |      |
| 629  | Qy | TCAGTGGCTTAATCAAGCTTCAGAAATATATATCCAGGACAAATGAAGAAAGAAATGGTAGA  | 688  |
| 751  | Db |   | 692  |
|      |    | TCAGTGGCTTAATGAGCTTCGAAATATATATCCAGGNCAACTGAAAGAAAGAAATGGTAGA   |      |
| 689  | Qy | GATACAGCAAGATCCAGTACAGAACACAGACGGCTGTGATAGAAATAGGGAACAACCT      | 748  |
| 691  | Db |   | 632  |
|      |    | GATACAGCAAGATCCAGTACAGAACACAGACGGCTGTGATAGAAATAGGGAACAACCT      |      |
| 749  | Qy | GTTTGAACCAACACGCTGAGCAACACGGCGGAAGTTAACTGATGTGGAAGCCCAAGTATTAAA | 808  |
| 631  | Db |   | 572  |
|      |    | GTTTGAACCAACACGCGAGCAACACGGCGGAAGTTAACTGATGTGGAAGCCCAAGTATTAAA  |      |
| 809  | Qy | TCAGACCAACGAGACTTGAACTTCAGCTCTTTGGAACTCCCTCTTCGACAAACAAATTGGA   | 868  |
| 571  | Db |   | 512  |
|      |    | TCAGACCAACGAGACTTGAACTTCAGCTCTTTGGAACTCCCTCTTCGACAAACAAATTGGA   |      |
| 869  | Qy | AAACAGATTTTGGACAGACACGATGAAATATAACAAATTGCAAGATAGACAGTTTCCT      | 928  |
| 511  | Db |   | 452  |
|      |    | AAACAGATTTTGGACACGACCAAGTGAAATATAACAAATTGCAAGATAGAAACAGTTTCCT   |      |
| 929  | Qy | AGAAAGAAAGTGCTAGCTATGGAAGACAAAGCACATCATCAACTACAGTCAATAAAAGA     | 988  |
| 451  | Db |   | 392  |
|      |    | AGAAAGAAAGTGCTAGCTATGGAAGACAAAGCACATCATCAACTACAGTCAATAAAAGA     |      |
| 989  | Qy | AGAGAAAGATCAGCTACAGGTGTAGTATCCAAGCAAAATTCATCATTTGAGAACTTAGA     | 1048 |
| 391  | Db |   | 332  |
|      |    | AGAGAAAGATCAGCTACAGGTGTAGTATCCAAGCAAAATTTCCATCATTTGAGAACTTAGA   |      |
| 1049 | Qy | AAAAAAATAGTGACTCCACGGTGAATAATTTCAGTTTCTTCAAAAGCAGCAACATGATCT    | 1108 |
| 331  | Db |   | 272  |
|      |    | AAAAAAATAGTGACTCCACGGTGAATAATTTCAGTTTCTTCAAAAGCAGCAACATGATCT    |      |
| 1109 | Qy | CATGGACACAGTTTAATAACTTACTGACTATGATGTCCACATCAAACTCAGTAAGGACCC    | 1168 |

|    |      |  |      |
|----|------|--|------|
| Qy | 1084 | TTCTTCAAAGCAGCAACATGATCTCATGGAGACAGTTATTAATCTTACTGACCTATGATGT      | 1144 |
| Db | 244  | TTCTTCAAGACGACCAACATGATCTCATGGAGACAGTTATTAATCTTACTGACCTATGATGT     | 303  |
| Qy | 1144 | CCACATCAAACCTCAGCTTAAGGACCCCACTGTGTCTAAAGAAAGAACAAATCAGCTTTCAGAG   | 1203 |
| Db | 304  | CCACATCAAACCT--CTAAGGACCCCACTGTGTCTAAAGAAAGAACAAATCAGCTTTCAGAG     | 360  |
| Qy | 1204 | ACTGTGCTGAAGTATTCAAATTCAGGACACACCAACAAATGGGATCTACACGTTTAACATTTCC   | 1263 |
| Db | 361  | ACTGTGCTGAAGTATTCAAATTCAGGACACACCAACCAAGATGGCATCTACACGTTTAACATTTCC | 420  |
| Qy | 1264 | CTTAATTTCTACAGAAGAGATCAAGCCCTACTGTGTGACATGGAGCTGGAGGAGGGGGTGGGA    | 1323 |
| Db | 421  | CTTAATTTCTACAGAAGAGATCAAGCCCTACTGTGTGACATGGAGCTGGAGGAGGGGGTGGGA    | 480  |
| Qy | 1324 | CAATTAATTCAGCGACGTGAGGATGGCAGCGTTGATTTTTTCAGAGGACCTTGAAAGAAATATA   | 1383 |
| Db | 481  | CAATTAATTCAGCGACGTGAGGATGGCAGCGTTGATTTTTTCAGAGGACCTTGAAAGAAATATA   | 540  |
| Qy | 1384 | AAGTGGGATTTGGTAAACCCCTTCAGGAGAAATATTGGCTGGGAAATGAGTTTGTTCGCAAC     | 1443 |
| Db | 541  | AAGTGGGATTTGGTAAACCCCTTCAGGAGAAATATTGGCTGGGAAATGAGTTTGTTCGCAAC     | 600  |
| Qy | 1444 | TGACTAATCAGCAACGCTATGTGCTTAAATACACCTTAAAGACTGGGAGGGGAATCAGG        | 1503 |
| Db | 601  | TGACTAATCAGCAACGCTATGTGCTTAAATACACCTTAAAGACTGGGAGGGGAATCAGG        | 660  |
| Qy | 1504 | CTTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAAATTAAGAGTTCAAC      | 1563 |
| Db | 661  | CTTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAAATTAAGAGTTCAAC      | 720  |
| Qy | 1564 | TTAAAGGACTTACAGGACAGCCGGCAAAATTAAGCAGCATCAGCCAAACCAAGGAAATGATT     | 1623 |
| Db | 721  | TTAAAGGACTTACAGGACAGCCGGCAAAAT--AGCAGCATCAGCCAAACCAAGGAAATGATT     | 779  |
| Qy | 1624 | TTAGCAAAAGGATGGAGACAAACGACAAATGTATTTGCAATGTCTCAAAATGCTCAACGTTACAG  | 1683 |
| Db | 780  | TTAGCAAAAGGATGGGAGACACACAAATGTATTTGCAATGTCTCAAAATGCTCAACGTTACAG    | 839  |
| Qy | 1684 | GAGGCTGGT--GGTTTGATGCATGTGGTGCTTTCCAACTTGAAACGGAATGTACTATCCACA     | 1741 |
| Db | 840  | GAGGCTGNTGGTNTTGATGCATGTGGTCTTTTCAACTTGAAACGGAATGTACTATCCACA       | 899  |
| Qy | 1742 | GAGGACAGAACAAATTAAGTTCAACGGCATTPAATGGTACTACTGGAAAGGCTCAGGCTA       | 1801 |
| Db | 900  | GAGGACAGACCAC--AATAAGTTCAACGGCATTTAATGGTACTACTTTGGAAGTCTACAGCTT    | 958  |
| Qy | 1802 | TT 1803  |      |
| Db | 959  | TT 960   |      |

|            |  |
|------------|--|
| RESULT     | 9  |
| BX391728/c |  |
| LOCUS      |  |
| DEFINITION | BX391728 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSOD1037YC20 3-PRIME, mRNA sequence.                |
| ACCESSION  | BX391728   |
| VERSION    | BX391728.1   |
| KEYWORDS   | GI:30619519  |
| SOURCE     | EST.   |
| ORGANISM   | Homo sapiens (human)   |
| AUTHORS    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| TITLE      | Li,W.B., Gruber,C., Jessee,J. and Polayes,D.<br>Full-length cDNA libraries and normalization<br>1 (bases 1 to 932)           |
| JOURNAL    | Contact: Genoscope   |
| COMMENT    | Genoscope - Centre National de Sequencage<br>2 rue Gaston Cremieux. CP 5706 - 91057 EVRY cedex - FRANCE                      |

|                       |   |   |                 |
|-----------------------|---|---|-----------------|
| Db                    | 271   | CATGGAGACAGTTTAATTAACCTTACTGACTATGATGTCACATCAACT-CTAGGACCC    | 215             |
| Qy                    | 1169  | CACGTGTTGCTAAAGAACAAATCAGCTTCAGAGACTGTGCTGAAGTATTCAAATCAGG    | 1228            |
| Db                    | 214   | CACGTGTTGCTAAAGAACAAATCAGCTTCAGAGACTGTGCTGAAGTATTCAAATCAGG    | 155             |
| Qy                    | 1229  | ACACACACAAATGGCATCTACACGTTAAACATTCCTTAATTTACAGAAGATCAAGGC     | 1288            |
| Db                    | 154   | ACACACACGAATGGCATCTACACGTTAAACATTCCTTAATTTACAGAAGATCAAGGC     | 95              |
| Qy                    | 1289  | CTACTGTGACATGAAGCTGAGAGAGCGGGTGAACAATTATTTCAGCGAGTGAAGATGG    | 1348            |
| Db                    | 94  | CTACTGTGACATGAAGCTGAGAGAGCGGGTGAACAATTATTTCAGCGAGTGAAGATGG    | 35              |
| Qy                    | 1349  | CAGCGTTGATTTTCAGAGGACTTGGAAAGATATA                            | 1383            |
| Db                    | 34  | CAGCGTT-ATTTTCAGAGGACGTGAAAGAAATAAA                           | 1               |
| RESULT 10             |   |   |                 |
| AY407059              |   |   |                 |
| LOCUS                 | AY407059  | 1213 bp DNA linear  | GSS 15-DEC-2003 |
| DEFINITION            | Pan troglodytes ANGPT2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.   |   |                 |
| ACCESSION             | AY407059  |   |                 |
| VERSION               | AY407059.1  | GI:39763030   |                 |
| KEYWORDS              | GSS.  |   |                 |
| SOURCE                | Pan troglodytes (chimpanzee)  |   |                 |
| ORGANISM              | Pan troglodytes   |   |                 |
| REFERENCE             | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. |   |                 |
| AUTHORS               | 1 (bases 1 to 1213)   |   |                 |
| TITLE                 | Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  |   |                 |
| JOURNAL               | Science   | 302 (5652), 1960-1963 (2003)                                  |                 |
| PUBMED                | 14671302  |   |                 |
| REFERENCE             | 2 (bases 1 to 1213)   |   |                 |
| AUTHORS               | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. |   |                 |
| TITLE                 | Direct Submission   |   |                 |
| JOURNAL               | Submitted (16-NOV-2003)   | Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA |                 |
| COMMENT               | This sequence was made by sequencing genomic exons and ordering them based on alignment.  |   |                 |
| FEATURES              | Location/Qualifiers   |   |                 |
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|                       | /mol_type="genomic DNA"   |   |                 |
|                       | /db_xref="taxon:9598"   |   |                 |
|                       | <1..>1213   |   |                 |
| gene                  | /gene="ANGPT2"  |   |                 |
|                       | /locus_tag="HCM2764"  |   |                 |
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| Query Match           | 35.08;  | Score 798.8; DB 9; Length 1213;                               |                 |
| Best Local Similarity | 83.8;   | Pred. No. 5.8e-209;   |                 |
| Matches               | 815; Conservative   | 0; Mismatches 158; Indels                                     | 0; Gaps 0;      |
| Qy                    | 873   | CAGATTTTGGACACAGCAGTGAATAAAACAAATTCGAAGATAAGAACAGTTTCCTAGAA   | 932             |
| Db                    | 241   | CAAGTGTGGAGACATCATGGAACAAACACTCAGTGGCTATGAAGATGTTTCCTAGAA     | 300             |
| Qy                    | 933   | AAGAAGTGTAGCTATGGAAGACAAGCAATCATCAATCCAACTACAGTCAATAAAGAAGAG  | 992             |
| Db                    | 301   | AAGAAGGTGTAGCTATGGAAGACAAGCAATCATCAATCCAACTACAGTCAATAAAGAAGAG | 360             |

|   |      |  |      |
|---|------|--|------|
| Qy  | 993  | AAAGATCAGCTACAGGTTGTAGTATCAAGCAAAATTCATTCATTTGAAGAACTAGAAAAA         | 1052 |
| Db  | 361  | AAAGATCAGCTACAGGTTGTAGTATCAAGCAAAATTCATTCATTTGAAGAACTAGAAAAA         | 420  |
| Qy  | 1053 | AAAATAGTGACTGCCACGGTGAATAATTCAGTTCTTCAAAGCAGCAACATGATCTCATG          | 1112 |
| Db  | 421  | AAAATAGTGACTGCCACGGTGAATAATTCAGTTCTTCAAAGCAGCAACATGATCTCATG          | 480  |
| Qy  | 1113 | GAGACAGTTAAATAACTTTACTGACTATGATGTCCACATCAAATTCAGCTACAGTAAAGGACCCCACT | 1172 |
| Db  | 481  | GAGACAGTTAAATAACTTTACTGACTATGATGTCCACATCAAATTCAGCTACAGTAAAGGACCCCACT | 540  |
| Qy  | 1173 | GTTCCTAAAGAAGACAAATTCAGCTTCAGAGACTGTGCTGAAGTATTCAAATCAGGACAC         | 1232 |
| Db  | 541  | NN       | 600  |
| Qy  | 1233 | ACCACAAATGGCATCTACAGCTTAACTCCCTAAATTCACAGAGAGATCAAGGCCCTAC           | 1292 |
| Db  | 601  | NN       | 660  |
| Qy  | 1293 | TGTGACATGAAGCTGAGGAGCGGTGCAAAATTTATTCAGCGACGTGAGGATGGCAGC            | 1352 |
| Db  | 661  | TGTGACATGAAGCTGAGGAGCGGTGCAAAATTTATTCAGCGACGTGAGGATGGCAGC            | 720  |
| Qy  | 1353 | GTTCGATTTTCAGAGGACTTGGAAAGAATAATAAGTGGGATTTGGTAAACCTTCAGGAGAA        | 1412 |
| Db  | 721  | GTTCGATTTTCAGAGGACTTGGAAAGAATAATAAGTGGGATTTGGTAAACCTTCAGGAGAA        | 780  |
| Qy  | 1413 | TATTTGGCTGGGAAATGAGTTTGTTCGCAACTGACTAAATCAGCAACGCTATGCTTTAAA         | 1472 |
| Db  | 781  | TATTTGGCTGGGAAATGAGTTTGTTCGCAACTGACTAAATCAGCAACGCTATGCTTTAAA         | 840  |
| Qy  | 1473 | ATACACTTAAAGACTCGGAAGGGAATGAGGCTTACTCATTTGTATGAACATTTCTATCTC         | 1532 |
| Db  | 841  | ATACACTTAAAGACTCGGAAGGGAATGAGGCTTACTCATTTGTATGAACATTTCTATCTC         | 900  |
| Qy  | 1533 | TCAAGTGAAGAACTCAATTTATAGGATTCACCTTTAAAGGACTTACAGGGAAGCGCGCAAA        | 1592 |
| Db  | 901  | TCAAGTGAAGAACTCAATTTATAGGATTCACCTTTAAAGGACTTACAGGGAAGCGCGCAAA        | 960  |
| Qy  | 1593 | ATAAGCAGCATCAGCAAACGAGAAATGATTTTAGCAAAAGGATGGAGACAAACGACAAA          | 1652 |
| Db  | 961  | ATAAGCAGCATCAGCAAACGAGAAATGATTTTAGCAAAAGGATGGAGACAAACGACAAA          | 1020 |
| Qy  | 1653 | TGTATTTGCAAAATGTTTCAAAATGCTAAACAGGAGGCTGGTGGTTGATGCATGTGGTCT         | 1712 |
| Db  | 1021 | TGTATTTGCAAAATGTTTCAAAATGCTAAACAGGAGGCTGGTGGTTGATGCATGTGGTCT         | 1080 |
| Qy  | 1713 | TCCAACTTGAACCGAATGTACTATCCACAGAGCGCAAAACAAATAAGTTTCAACGGCATTT        | 1772 |
| Db  | 1081 | TCCAACTTGAACCGAATGTACTATCCACAGAGCGCAAAACAAATAAGTTTCAACGGCATTT        | 1140 |
| Qy  | 1773 | AAATGGTACTACTGGAAGGCTCAGGCTATTCGCTCAAGGCCCAACCAATGATGATCCGA          | 1832 |
| Db  | 1141 | AAATGGTACTACTGGAAGGCTCAGGCTATTCGCTCAAGGCCCAACCAATGATGATCCGA          | 1200 |
| Qy  | 1833 | CCAGCAGATTCT   | 1845 |
| Db  | 1201 | CCAGCAGATTCT   | 1213 |
| RESULT 11   |      |  |      |
| CB528341/c  |      |  |      |
| LOCUS   |      |  |      |
| DEFINITION  |      |  |      |
| UI-H-FT2-bjg-j-05-0-UI.s1 NCI CGAP FT2 Homo sapiens CDNA clone    |      |  |      |
| UI-H-FT2-bjg-j-05-0-UI 3', mRNA sequence.                         |      |  |      |
| ACCESSION   |      |  |      |
| CB528341  |      |  |      |
| VERSION   |      |  |      |
| CB528341.1 GI:29387926  |      |  |      |
| KEYWORDS  |      |  |      |
| EST.  |      |  |      |
| SOURCE  |      |  |      |
| Homo sapiens (human)  |      |  |      |
| ORGANISM  |      |  |      |
| Homo sapiens  |      |  |      |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |      |  |      |
| Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.        |      |  |      |
| CB528341  |      |  |      |
| 721 bp  |      |  |      |
| mRNA  |      |  |      |
| linear  |      |  |      |
| EST 05-AUG-2004   |      |  |      |

|                               |  |
|-------------------------------|--|
| REFERENCE<br>AUTHORS<br>TITLE | 1 (bases 1 to 721)<br>NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .<br>National Cancer Institute, Cancer Genome Anatomy Project (CGAP),<br>Tumor Gene Index   |
| JOURNAL<br>COMMENT            | Unpublished (1997)<br>Contact: Robert Strausberg, Ph.D.<br>Email: <a href="mailto:cgaps-rc@mail.nih.gov">cgaps-rc@mail.nih.gov</a><br>Tissue Procurement: Dr. Gary W. Hunninghake, U of I<br>cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa<br>DNA Sequencing by: Dr. M. Bento Soares, University of Iowa<br>Clone Distribution: Distribution information can be found at<br><a href="http://genome.uiowa.edu/distribution/cgap.html">http://genome.uiowa.edu/distribution/cgap.html</a><br>Seq primer: M13 FORWARD<br>POLYA=Yes  |
| FEATURES<br>source            | Location/Qualifiers<br>1..721<br>/organism="Homo sapiens"<br>/mol_type="mRNA"<br>/db_xref="taxon:9606"<br>/clone="UI-H-FT2-bjg-j-05-0-UI"<br>/tissue_type="Alveolar Macrophage"<br>/dev_stage="Adult"<br>/lab_host="DH10B (Life Technologies)"<br>/clone_lib="NCI CGAP FT2"<br>/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a<br>modified polylinker; Site 1: EcoR I; Site 2: Not I;<br>NCI CGAP FT2 is a subcloned cDNA library constructed from<br>a pool of 81 RNA samples from Alveolar Macrophages<br>challenged with different treatments. The mRNA samples<br>were a mixture of these conditions (times refer to<br>incubations following isolation by bronchoalveolar lavage)<br>(some normal donor macrophages were cultured in some of<br>the conditions, other donor macrophages in different<br>conditions). The mRNA samples were pooled for library<br>construction. Control 0 hours; control 3 hours; control 24<br>hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;<br>PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella<br>moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph<br>aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours;<br>Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; wt<br>Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt<br>adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24<br>hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;<br>wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.<br>The library was subcloned according to Bonaldo, Lennon<br>and Soares, Genome Research, 6:791-806, 1996. The tissue<br>was provided by Dr. Gary W. Hunninghake of the University<br>of Iowa.<br>TAG TISSUE=Human Lung Alveolar Macrophage<br>TAG_LIB=UI-H-FT2<br>TAG_SEQ=GGCCATGCCG" |
| ORIGIN                        | Query Match 29.6%; Score 675.8; DB 6; Length 721;<br>Best Local Similarity 99.7%; Pred. No. 5e-175;<br>Matches 677; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  |
| Qy                            | 1604 CAGCCAAACGAGAAATGATTTTACACAAAGATGGAGACACCAAAATGATTTGCAA 1663  |
| Db                            | 721 CAGCCAAACGAGAAATGATTTTACACAAAGATGGAGACACCAAAATGATTTGCAA 662  |
| Qy                            | 1664 ATGTTTCAAAATGCTAACAGAGGCTGGTGGTTTGATGTCATGGTCTTCCAACTTCAA 1723  |
| Db                            | 661 ATGTTTCAAAATGCTAACAGAGGCTGGTGGTTTGATGTCATGGTCTTCCAACTTCAA 602  |
| Qy                            | 1724 CGGAATGACTATCCACAGAGCGAGACACAAATTAAGTTCAACGGCATTAATGGTACTA 1783   |
| Db                            | 601 CGGAATGACTATCCACAGAGCGAGACACAAATTAAGTTCAACGGCATTAATGGTACTA 542   |
| Qy                            | 1784 CTGGAAGAGGCTCAGGCTATTTCGCTCAAGGCCACCAACCATGATGATCCGACGAGATTT 1843   |
| Db                            | 541 CTGGAAGAGGCTCAGGCTATTTCGCTCAAGGCCACCAACCATGATGATCCGACGAGATTT 482   |
| Qy                            | 1844 CTAAACATCCAGTCCAGCTGAGGAACTGCTCGAATATTTTCAAGAACTTAAGCCAG 1903   |
| Db                            | 481 CTAAACATCCAGTCCAGCTGAGGAACTGCTCGAATATTTTCAAGAACTTAAGCCAG 422   |
| Qy                            | 1904 TGCACCTGAAAGTCAACGGCTGCGCAGCTGTCTCTTCCACCAAGAGGGGCTGTGCTCGG 1963  |
| Db                            | 421 TGCACCTGAAAGTCAACGGCTGCGCAGCTGTCTCTTCCACCAAGAGGGGCTGTGCTCGG 362  |
| Qy                            | 1964 TCGTGAACGGGACCCACATGCTCCAGATTAGAGCTGTAACTTATTCATTAACTTGCA 2023  |
| Db                            | 361 TCGTGAACGGGACCCACATGCTCCAGATTAGAGCTGTAACTTATTCATTAACTTGCA 302  |
| Qy                            | 2024 TCATTTAAGCGGACCAAGCAAGCCCTAAACATCCATATTTGATTAGACAGAACACCT 2083  |
| Db                            | 301 TCATTTAAGCGGACCAAGCAAGCCCTAAACATCCATATTTGATTAGACAGAACACCT 242  |
| Qy                            | 2084 ATGCAAGATGAACCCGAGGCTGAGAAATCAGACTGACAGTTTACAGACGCTGTGTGCA 2143   |
| Db                            | 241 ATGCAAGATGAACCCGAGGCTGAGAAATCAGACTGACAGTTTACAGACGCTGTGTGCA 182   |
| Qy                            | 2144 ACCAAGATGTTATGTGCAAGTTTATCAGTAATACTGGAACACAGAACTATGTTA 2203   |
| Db                            | 181 ACCAAGATGTTATGTGCAAGTTTATCAGTAATACTGGAACACAGAACTATGTTA 122   |
| Qy                            | 2204 TACAATACAGATCATCTTGGAACTGCAATTTCTTGAGCACTGTTTATACACTGTGTAAT 2263  |
| Db                            | 121 TACAATACAGATCATCTTGGAACTGCAATTTCTTGAGCACTGTTTATACACTGTGTAAT 62   |
| Qy                            | 2264 ACCATATGTCCTGAATTC 2282   |
| Db                            | 61 ACCATATGTCCTGAATTC 43   |
| RESULT 12                     |  |
| LOCUS                         | AI862415 735 bp mRNA linear EST 26-AUG-1999  |
| DEFINITION                    | td16b10.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2075803 3', similar to TR:O15123 O15123 ANGIOPOIETIN-2, mRNA sequence.  |
| ACCESSION                     | AI862415   |
| VERSION                       | AI862415.1 GI:5526522  |
| KEYWORDS                      | EST.   |
| SOURCE                        | Homo sapiens (human)   |
| ORGANISM                      | Homo sapiens   |
| REFERENCE                     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |
| AUTHORS                       | 1 (bases 1 to 735)   |
| TITLE                         | NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .<br>National Cancer Institute, Cancer Genome Anatomy Project (CGAP),<br>Tumor Gene Index<br>Unpublished (1997)<br>Contact: Robert Strausberg, Ph.D.<br>Email: <a href="mailto:cgaps-rc@mail.nih.gov">cgaps-rc@mail.nih.gov</a><br>Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.<br>cDNA Library Preparation: M. Bento Soares, Ph.D.<br>cDNA Library Arrayed by: Greg Lennon, Ph.D.<br>DNA Sequencing by: Washington University Genome Sequencing Center<br>Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://www-bio.llnl.gov/bbrp/image/image.html">www-bio.llnl.gov/bbrp/image/image.html</a><br>Seq primer: -40UP from Gibco<br>High quality sequence stop: 475.   |
| JOURNAL                       | Location/Qualifiers  |
| COMMENT                       | 1..735<br>/organism="Homo sapiens"<br>/mol_type="mRNA"<br>/db_xref="taxon:9606"<br>/clone="IMAGE:2075803"<br>/tissue_type="colon tumor, RER+"<br>/lab_host="DH10B"<br>/clone_lib="NCI CGAP Col6"<br>/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a   |
| FEATURES                      | source   |

modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Plasmid DNA from the normalized library NCI\_CGAP Col10 was  
prepared, and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(cloneids 1057416-1061255, and 1144584-1145351).  
Subtraction by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

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Query Match      29.1%; Score 663.4; DB 1; Length 735;
Best Local Similarity 97.4%; Pred. No. 1.3e-171;
Matches 684; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 1581 ACAGCGCGCAAAATAGCAGCATCAGCCAAACAGAGAAATGATTTAGCACAAGATGGA 1640
DB |||||
DB 735 ACAGCGCGCAAAATAGCAGCATCAGCCAAACAGAGATGATTTAGCACAAGATGNA 576
QY 1641 GACACGCAAAATGATTTGCAAAATGTTCAAAATGCTTAACAGGAGGCTGGTGGTTGAT 1700
DB |||||
DB 675 GACAAAGCAAAATAGTATTTGCAAAATGTTCAAAATGCTTAACAGGAGGCTGGTGGTTGAT 616
QY 1701 GCATGTGTCCTTCCAACTTGAACGGAATGTAATCCACAGAGGAGGCTGGTGGTTGAT 1760
DB |||||
DB 615 GCATGTGTCCTTCCAACTTGAACGGAATGTAATCCACAGAGGAGGCTGGTGGTTGAT 557
QY 1761 TTCAACGCGCATTAATGTTGCTTACTGGAAGGCTCAGGCTATTCGCTCAAGGCCACAACC 1820
DB |||||
DB 556 TTCAACGCGCATTAATGTTGCTTACTGGAAGGCTCAGGCTATTCGCTCAGGCCACAACC 497
QY 1821 ATGATGATCCGACGAGCATTTCTAAACATCCAGTCCACCTGAGGAACTGCTCGAAC 1880
DB |||||
DB 496 ATGATGATCCGACGAGCATTTCTAAACATCCAGTCCACCTGAGGAACTGCTCGAAC 437
QY 1881 TATTTTCAAGACTTAAGCCAGTGCACCTGAAGTCAGGCTGCCACTGTCTCTTC 1940
DB |||||
DB 436 TATTTTCAAGACTTAAGCCAGTGCACCTGAAGTCAGGCTGCCACTGTCTCTCTTC 377
QY 1941 CACCACAGAGGCGGTGTGTCGGTGTGTCAGCGGACCCACATGCTCCAGATTAGACCTGT 2000
DB |||||
DB 376 CACCACAGAGGCGGTGTGTCGGTGTGTCAGCGGACCCACATGCTCCAGATTAGACCTGT 317
QY 2001 AAACHTTATCACTTAACTTGATCACTTAAACGAGCAAAAGCAAGACCCCTAAACATCCAT 2060
DB |||||
DB 316 AAACHTTATCACTTAACTTGATCACTTAAACGAGCAAAAGCAAGACCCCTAAACATCCAT 257
QY 2061 AATTGTGATTAGACAGAACACCTATGCAAGATGAACCGGCTGAGAATCAGACTGAC 2120
DB |||||
DB 256 AATTGTGATTAGACAGAACACCTATGCAAGATGAACCGGCTGAGAATCAGACTGAC 197
QY 2121 AGTTTACAGACGCTGTGTCAACCAAGAAATGTTATGTGCAAGTATATCAGTAATAAC 2180
DB |||||
DB 196 AGTTTACAGACGCTGTGTCAACCAAGAAATGTTATGTGCAAGTATATCAGTAATAAC 137
QY 2181 TGGAAAACAGAACACTTATGTTATACATACAGATCATCTTGGAACTGCAATCTCTGAG 2240
DB |||||
DB 136 TGGAAAACAGAACACTTATGTTATACATACAGATCATCTTGGAACTGCAATCTCTTGGAG 77
QY 2241 CACTGTTTATACACTGTGTAATATCCCATATGCTCTGGAATTC 2282
DB |||||
DB 76 CACTGTTTATACACTGTGTAATATCCCATATGCTCTGGAATTC 35
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RESULT 13  
BG714406  
LOCUS BG714406 696 bp mRNA linear EST 08-MAY-2001  
DEFINITION 60266930F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:4792831 5',  
mRNA sequence.  
ACCESSION BG714406  
VERSION BG714406.1 GI:13993337  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 696)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLNM10671 row: k column: 08

High quality sequence stop: 677.

## FEATURES

## source

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1..696
Location/Qualifiers
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/mol_type="mRNA"
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/clone_image="IMAGE:4792831"
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/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/notes="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dr primed using primer 5'-TTTTTTTATTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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## ORIGIN

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Query Match      28.6%; Score 652.8; DB 4; Length 696;
Best Local Similarity 98.7%; Pred. No. 1.1e-168;
Matches 679; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 162 TTACTGCATGCTCGAGAGAAACAGCAGTAGTAAAAACCCAGGTTTGCTACTGAAAAAGAGG 221
DB |||||
DB 8 TTACTGCATGCTCGAGAGAAACAGCAGTAGTAAAAACCCAGGTTTGCTACTGAAAAAGAGG 67
QY 222 AAAGAGAAGCTTTTCATTGACGGACCCAGCCATGCGAGCGTAGCAGCCCTGGTTTCAGA 281
DB |||||
DB 68 AAAGAGAAGCTTTTCATTGACGGACCCAGCCATGCGAGCGTAGCAGCCCTGGTTTCAGA 127
QY 282 CGGCAGCAGCTCGGAGCTCTGGACGTGTGTTTGCCTCAAGTTTGCTAAGCTGCTGGTTT 341
DB |||||
DB 128 CGGCAGCAGCTCGGAGCTCTGGACGTGTGTTTGCCTCAAGTTTGCTAAGCTGCTGGTTT 187
QY 342 ATTACTGAAGAAAGAAATGTCAGATGTTTCTTTACTCTGAGCTGTGATCTTGCTTG 401
DB |||||
DB 188 ATTACTGAAGAAAGAAATGTCAGATGTTTCTTTACTCTGAGCTGTGATCTTGCTTG 247
QY 402 GCCCGAGCCTATACAACTTTCCGAAGAGCATGGAAGCATAGGAAGCAAGCAATATCAG 461
DB |||||
DB 248 GCCCGAGCCTATACAACTTTCCGAAGAGCATGGAAGCATAGGAAGCAAGCAATATCAG 307
QY 462 GTCCAGCATGGGTCTGTCAGCTACACTTTCTCTCCCGCAGAGATGGACAACTGCCGCTCT 521
DB |||||
DB 308 GTCCAGCATGGGTCTGTCAGCTACACTTTCTCTCCCGCAGAGATGGACAACTGCCGCTCT 367
QY 522 TCCTCCAGCCCTACGTTGTCATGCTGTGAGAGGAGACGCCGCTCGAATACGATGAC 581
DB |||||
DB 368 TCCTCCAGCCCTACGTTGTCATGCTGTGAGAGGAGACGCCGCTCGAATACGATGAC 427
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DB |||||
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|-----------------------|-----|---|------|
| Db                    | 428 | TCGGTCGAGAGCGCTGCAAGTGTGGAGAACATCATCGAAGAAACAACTCAGTGGCTAATG        | 487  |
| QY                    | 642 | AAGCTTCAGAAATATATCCAGGACCAACATGAAGA-AAGAAATGGTAGAGATACAGCAGA-       | 699  |
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| QY                    | 700 | ATCGAGTACAGAACCGACGGCTGTGATGATAGAAATAGGAGCAAAACCTGTTGAACCAA         | 759  |
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| QY                    | 820 | GACTTGAACCTCAGCTCTTGGAAACACTC 847                                   |      |
| Db                    | 668 | GACTTGAACCTCAGCTCTTGGAAACACTC 695                                   |      |
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| DEFINITION            |     | genomic survey sequence.  |      |
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| ORGANISM              |     | Mus musculus  |      |
| REFERENCE             |     |   |      |
| AUTHORS               |     | 1 (bases 1 to 1218)   |      |
|                       |     | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., |      |
|                       |     | Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,     |      |
|                       |     | Ferrera, S., Wang, C., Zheng, X.H., White, T.J., Sninsky, J.J.,     |      |
|                       |     | Adams, M.D. and Cargill, M.   |      |
| TITLE                 |     | Inferring nonneutral evolution from human-chimp-mouse orthologous   |      |
|                       |     | gene trios  |      |
| JOURNAL               |     | Science 302 (5652), 1960-1963 (2003)                                |      |
| PUBMED                |     | 14671302  |      |
| REFERENCE             |     |   |      |
| AUTHORS               |     | 2 (bases 1 to 1218)   |      |
|                       |     | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., |      |
|                       |     | Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,     |      |
|                       |     | Ferrera, S., Wang, C., Zheng, X.H., White, T.J., Sninsky, J.J.,     |      |
|                       |     | Adams, M.D. and Cargill, M.   |      |
| TITLE                 |     | Direct Submission   |      |
| JOURNAL               |     | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,        |      |
| COMMENT               |     | Rockville, MD 20850, USA  |      |
|                       |     | This sequence was made by sequencing genomic exons and ordering     |      |
|                       |     | them based on alignment.  |      |
| FEATURES              |     |   |      |
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| QY                    | 933 | AAGAGGTGTAGTATGGAAGACAGACATATCCACTACATCAATTAAGAGAGAG                | 992  |
| Db                    | 301 | CAGAAAGTTCTGGACATGGAGGGGCAAGCAGCAGCGAGCTTACAGTCCATGAAGGACAG         | 360  |
| QY                    | 993 | AAAGATCAGCTACAGGTGTTAGTATCCAAAGCAAAATTCATCATTTGAAGAACTAGAAAAA       | 1052 |

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| Db         | 421  | AAGCTGGTCAGAGCCACCGGTCAACAACTCGCTCCTTCAGAAAGCAGCAGCATGACCTAATG      | 480  |
| QY         | 1113 | GAGACAGTTAATACTTACTGACTATGATGTCCACATCAAACTCAACTCAGCTAAGGACCC        | 1169 |
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| QY         | 1170 | ACTGTTGCTAAAGAAAGCAAAATCAGCTTCAGAGACTGTGCTGAAGTATTCAATCAGGA         | 1229 |
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| QY         | 1230 | CACACCAAAATGGCATCTACAGTTTAAATTCCTTAATCTTACAGAAAGATCAAGGCC           | 1289 |
| Db         | 601  | CTCACCCAGTGGCATCTACACACTGACCTTCCCACTCCACAGAGAGATCAAGGCC             | 660  |
| QY         | 1290 | TACTGTGACATGAAGCTGGAGAGCGGGTGGACAATTAATTATTCAGGCACTGAGGATGGC        | 1349 |
| Db         | 661  | TACTGTGACATGACCGTGGGTGGAGAGGGTGGACAGTCAATCCAAACACCGAGAAGATGGC       | 720  |
| QY         | 1350 | AGCGTTGATTTTCAGAGGACTTGGAAAGATATAAAGTGGATTTCGTAAACCTTCAGGA          | 1409 |
| Db         | 721  | AGTGTGGACTTCCAGAGGACGTGGAAAGAAATACAAAGAGGGCTTCGGAGCCCTCTGGGA        | 780  |
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| Db         | 781  | GAGTACTGCTGGGCAATGAGTTTGTCTCCAGCTGACCGGTGAGCACCGCTACGTGCTT          | 840  |
| QY         | 1470 | AAAATACACTTAAAGACTGGGAAGGAATGAGGCTTACTCATTTGATGAACAATTTCTAT         | 1529 |
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|            |      | IMAGE:2359934.3, similar to TR:077802.077802 ANGIOPOIETIN-2 ;, mRNA |      |
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| ACCESSION  |      | AI809922  |      |
| VERSION    |      | AI809922.1 GI:5396488   |      |
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| SOURCE     |      | Homo sapiens (human)  |      |
| ORGANISM   |      | Homo sapiens  |      |
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|            |      | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.          |      |

REFERENCE 1 (bases 1 to 647)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
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 libraries (fetal lung NBH19W, testis NHT, and B-cell  
 NCI CGAP GCBI) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 I.M.A.G.E. clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 26.8%; Score 611.8; DB 1; Length 647;  
 Best Local Similarity 99.7%; Pred. No. 2.4e-157;  
 Matches 613; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 QY 1788 AAAGGCTCAGGCTATTCGCTCAAGGCCCAACCATGATGATCGGACCGACGATTTCTAA 1847  
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 QY 1848 ACATCCAGTCCACCTGAGGAACCTGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCA 1907  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 02:51:04 ; Search time 2039.78 Seconds

(without alignments)  
7240.933 Million cell updates/sec

Title: US-10-603-293-5

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Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 2          | 2282  | 100.0       | 2282   | 14 | US-10-186-817-5 |
| 3          | 2282  | 100.0       | 2282   | 14 | US-10-225-060-5 |
| 4          | 2282  | 100.0       | 2282   | 15 | US-10-321-332-5 |
| 5          | 2282  | 100.0       | 2282   | 16 | US-10-179-615-5 |
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| 7          | 2282  | 100.0       | 2282   | 21 | US-10-603-293-5 |

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|------|--------|-------|--------|----|--------------------|-------------------|
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| 9    | 2269   | 99.4  | 2269   | 9  | US-09-998-831-3    | Sequence 3, Appli |
| 10   | 2269   | 99.4  | 2269   | 10 | US-09-998-833-3    | Sequence 3, Appli |
| 11   | 2269   | 99.4  | 2269   | 15 | US-10-101-510-460  | Sequence 460, App |
| 12   | 2269   | 99.4  | 2269   | 16 | US-10-373-561-3    | Sequence 3, Appli |
| 13   | 2269   | 99.4  | 2269   | 19 | US-10-317-803-18   | Sequence 18, Appl |
| 14   | 2269   | 99.4  | 2269   | 19 | US-10-789-222-33   | Sequence 33, Appl |
| 15   | 2269   | 99.4  | 2269   | 20 | US-10-827-759A-2   | Sequence 2, Appli |
| 16   | 2269   | 99.4  | 2269   | 21 | US-10-988-245-3    | Sequence 3, Appli |
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| 18   | 2269   | 99.4  | 2269   | 22 | US-10-712-124-103  | Sequence 103, App |
| 19   | 2233.6 | 97.9  | 2384   | 13 | US-10-044-090-23   | Sequence 23, Appl |
| 20   | 2233.6 | 97.9  | 2384   | 16 | US-10-131-013-250  | Sequence 250, App |
| 21   | 2230.4 | 97.7  | 2351   | 13 | US-10-044-080-24   | Sequence 21, Appl |
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| 23   | 2214.6 | 97.0  | 2642   | 21 | US-10-852-335A-56  | Sequence 56, Appl |
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| 28   | 1186.6 | 52.0  | 1387   | 10 | US-09-832-355A-95  | Sequence 95, Appl |
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| 32   | 1068.8 | 46.8  | 2424   | 19 | US-10-317-803-11   | Sequence 11, Appl |
| 33   | 1068.8 | 46.8  | 2424   | 19 | US-10-789-222-34   | Sequence 34, Appl |
| 34   | 1068.8 | 46.8  | 2424   | 20 | US-10-827-759A-5   | Sequence 5, Appli |
| 35   | 1068.2 | 46.8  | 2475   | 21 | US-10-764-420-1571 | Sequence 1571, Ap |
| 36   | 898.6  | 39.4  | 1497   | 14 | US-10-225-060-19   | Sequence 19, Appl |
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| 38   | 748.6  | 32.8  | 1488   | 14 | US-10-225-060-25   | Sequence 25, Appl |
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| 40   | 598    | 26.2  | 62705  | 19 | US-10-317-803-4    | Sequence 4, Appli |
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| C 42 | 595.6  | 26.1  | 240825 | 19 | US-10-468-582-1    | Sequence 1, Appli |
| C 43 | 595.6  | 26.1  | 240825 | 24 | US-11-028-971-1    | Sequence 1, Appli |
| C 44 | 551.6  | 24.2  | 2146   | 13 | US-10-179-744-3    | Sequence 3, Appli |
| 45   | 551.6  | 24.2  | 2146   | 14 | US-10-186-817-3    | Sequence 3, Appli |

ALIGNMENTS

RESULT 1

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; Publication No. US20020173627A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Samuel et al.  
; TITLE OF INVENTION: TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF  
; FILE REFERENCE: REG 330-F-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/179,744  
; CURRENT FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: US/08/817,318  
; PRIOR FILING DATE: 1999-09-16  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 2282  
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; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Unknown Organism  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (357)...(1847)  
; US-10-179-744-5

Query Match 100.0%; Score 2282; DB 13; Length 2282;  
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Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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421 TTCCGGAAGAGCATGGACAGCATAGGAAGAAAGCAATATCAGGTCCAGCATGGTCTTGCA 480  
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481 GCTACACTTCTCTGTCGACAGATGGACAACTGCGCGCTTCTCCAGCCCTTACGTGT 540  
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601 TCGTGAGAACATCATGGAAAAACAACACTCAGTGGCTAATGAAGCTTGAGATTATATCC 660  
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661 AGGACAACATAGGAAGAAATGTTAGATACAGCAGAAATGCAAGATCCAGTACAGACCGG 720  
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1441 AACTGACTAATCAGGACAGCTATGTGCTTAAATAACA CACTTAAAGACTGGGAGGGAATG 1500  
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Db 2221 TGGAACTGCAATCTCTGAGCACTGTTTATACACTGTGTAAATACCAATATGTCCTGAAT 2280  
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QY 2281 TC 2282  
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Db 2281 TC 2282

## RESULT 2

US-10-186-817-5  
; Sequence 5, Application US/10186817  
; Publication No. US20030040463A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Samuel et al.  
; TITLE OF INVENTION: Tie-2 Ligands, Methods of Making and Uses Thereof  
; FILE REFERENCE: REG 330-G-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/186,817  
; PRIOR FILING DATE: 2002-07-01  
; CURRENT APPLICATION NUMBER: US/08/930,721  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: PCT/US96/04806  
; PRIOR FILING DATE: 1996-04-05  
; PRIOR APPLICATION NUMBER: PCT/US95/12935  
; PRIOR FILING DATE: 1995-10-06  
; PRIOR APPLICATION NUMBER: 08/418,595  
; PRIOR FILING DATE: 1996-04-05  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 2282  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (357)..(1844)  
US-10-186-817-5

Query Match 100.0%; Score 2282; DB 14; Length 2282;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 TCTGGGAGAGAGAAACAAGGACCGTGAAGCTGCTCTGTAAAGCTGACACAGCCCTC 120  
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QY 2281 TC 2282
Db 2281 TC 2282
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RESULT 3
US-10-225-060-5
; Sequence 5, Application US/10225060
; Publication No. US20030092891A1
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE OF INVENTION: Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2282
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (357)..(1844)
; OTHER INFORMATION:
US-10-225-060-5
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Query Match 100.0%; Score 2282; DB 14; Length 2282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 CCAAGTGAAGCAGGACTGTTCTTCCACTGCAATCTGACAGTTTACTGCTGCTGGAGAG 180
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Db 541 CCAATGCTGTGAGAGGACCGCGCTCGAATACGATGACTCGGTGAGAGGCTGCAAG 600
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QY 841 AACACTCCCTCTCGACAAACAAATTTGAAAAACAGATTTTGGACACAGACCAAGTGAATAA 900
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QY 901 ACAAAATTCAGATGAAGAACAGTTCCTTAGAAAAGAGGTGCTAGCTATGGAAGACAAGC 960
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|----|------|--|------|
| Db | 901  | ACAAAATTGCAAGATAAAGACAGTTTCTCTGAAAGAAAGGTGCTAGCTATGGAAGACAAGC  | 960  |
| Qy | 961  | ACATCATCCAACTACAGTCAATTAAGAAGAGAGAAAGATCAGCTTACAGGTGTAGTATCCA  | 1020 |
| Db | 961  | ACATCATCCAACTACAGTCAATTAAGAAGAGAGAAAGATCAGCTTACAGGTGTAGTATCCA  | 1020 |
| Qy | 1021 | AGCAAAATTCATCATATTGAAGAACTAGAAAAAAAATAGTGACTGCGCAGCGTGAAATAAT  | 1080 |
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| Qy | 1081 | CAGTTCTTCAAAAGCAGCAACATGATCTCATGAGACAGTTAAATACTTATGACTATGA     | 1140 |
| Db | 1081 | CAGTTCTTCAAAAGCAGCAACATGATCTCATGAGACAGTTAAATACTTATGACTATGA     | 1140 |
| Qy | 1141 | TGTTCCACATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAGAGAGACAAATCAGCTTCA  | 1200 |
| Db | 1141 | TGTTCCACATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAGAGAGACAAATCAGCTTCA  | 1200 |
| Qy | 1201 | GAGACTGTGCTGAAGTATTCAAATCAGGACACACCACAAATGCGCATCTACACGTTAAACAT | 1260 |
| Db | 1201 | GAGACTGTGCTGAAGTATTCAAATCAGGACACACCACAAATGCGCATCTACACGTTAAACAT | 1260 |
| Qy | 1261 | TCCTTAATCTCAGAGAGAGATCAAGCCCTACTGTGTGACATGGAAGCTGGAGGAGCGGGT   | 1320 |
| Db | 1261 | TCCTTAATCTCAGAGAGAGATCAAGCCCTACTGTGTGACATGGAAGCTGGAGGAGCGGGT   | 1320 |
| Qy | 1321 | GGACAAATATTCAGCGACGTCAGGATGGCAGCGTTGATTTTCAGAGCATCTGGAAGAAT    | 1380 |
| Db | 1321 | GGACAAATATTCAGCGACGTCAGGATGGCAGCGTTGATTTTCAGAGCATCTGGAAGAAT    | 1380 |
| Qy | 1381 | ATAAGTGGGATTTGGTAAACCCCTTCAGGAGAAATATGGCTGGCAATAGCTTTGTTTCG    | 1440 |
| Db | 1381 | ATAAGTGGGATTTGGTAAACCCCTTCAGGAGAAATATGGCTGGCAATAGCTTTGTTTCG    | 1440 |
| Qy | 1441 | AACGTACTAATCAGCAACCGCTATGTGCTTAAAAATACACCTTAAAGACTGGGAAGGAATG  | 1500 |
| Db | 1441 | AACGTACTAATCAGCAACCGCTATGTGCTTAAAAATACACCTTAAAGACTGGGAAGGAATG  | 1500 |
| Qy | 1501 | AGGCTTACTCATTTGTATGAACATTTCTATCTCTCAAGTGAAGACACTCAATATAGGATTC  | 1560 |
| Db | 1501 | AGGCTTACTCATTTGTATGAACATTTCTATCTCTCAAGTGAAGACACTCAATATAGGATTC  | 1560 |
| Qy | 1561 | ACCTTAAAGGACTTACAGGGACACCGCGCAAAATAAGCAGCATCAGCCAAACCAGGAAATG  | 1620 |
| Db | 1561 | ACCTTAAAGGACTTACAGGGACACCGCGCAAAATAAGCAGCATCAGCCAAACCAGGAAATG  | 1620 |
| Qy | 1621 | ATTTTAGCACAAAGGATGGAGACAACGACAAATGTATTTGCAATGTTCACAAATGCTAA    | 1680 |
| Db | 1621 | ATTTTAGCACAAAGGATGGAGACAACGACAAATGTATTTGCAATGTTCACAAATGCTAA    | 1680 |
| Qy | 1681 | CAGAGGCTGTGTGTTGATGCAATGTGGTCTTCCAACCTTGAAACGGAATCTACTATCCAC   | 1740 |
| Db | 1681 | CAGAGGCTGTGTGTTGATGCAATGTGGTCTTCCAACCTTGAAACGGAATCTACTATCCAC   | 1740 |
| Qy | 1741 | AGAGCAGAACACAAATAAGTTCAACGCGATTAAATGCTACTCTGAAAGGGCTCAGGCT     | 1800 |
| Db | 1741 | AGAGCAGAACACAAATAAGTTCAACGCGATTAAATGCTACTCTGAAAGGGCTCAGGCT     | 1800 |
| Qy | 1801 | ATTTCGCTCAAGGCCACAAACCATGATGATCGGACAGAGATTTCTAAACATCCAGTCCA    | 1860 |
| Db | 1801 | ATTTCGCTCAAGGCCACAAACCATGATGATCGGACAGAGATTTCTAAACATCCAGTCCA    | 1860 |
| Qy | 1861 | CCTGAGGACGTCTCGAATCTATTTTCAAGACATTAAGCCAGTGCACTGAAAGTCAAGG     | 1920 |
| Db | 1861 | CCTGAGGACGTCTCGAATCTATTTTCAAGACATTAAGCCAGTGCACTGAAAGTCAAGG     | 1920 |
| Qy | 1921 | CTGGCAGCTGTCTCTCTTCCACACACAGAGGCGGTGTGCTCGGTGCTGACGGGACCCACA   | 1980 |
| Db | 1921 | CTGGCAGCTGTCTCTCTTCCACACACAGAGGCGGTGTGCTCGGTGCTGACGGGACCCACA   | 1980 |
| Qy | 1981 | TGCTCCAGATTAGAGCCCTGTAAACTTTTATCATCTTAACTTGTCATCATCTTAAACGGA   | 2040 |

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|---|------|--|------|
| Db  | 1981 | TGCTCCAGATTAGAGCCTGTAAACTTTATCACTTAAACTTTGCATCACTTAAACGGACCAA      | 2040 |
| Qy  | 2041 | GCAAGACCCCTAAACATCCATAAATTTGATTAGACAGAACACCTTATGCAAAAGATGAACCCG    | 2100 |
| Db  | 2041 | GCAAGACCCCTAAACATCCATAAATTTGATTAGACAGAACACCTTATGCAAAAGATGAACCCG    | 2100 |
| Qy  | 2101 | AGGCTGAGAATACAGACTGACAGTTTACAGACGGCTGCTGTCAAAACAGAAATGTTATGTG      | 2160 |
| Db  | 2101 | AGGCTGAGAATACAGACTGACAGTTTACAGACGGCTGCTGTCAAAACAGAAATGTTATGTG      | 2160 |
| Qy  | 2161 | CAAGTTTATCAGTAAATAAATCTGGAAAAACAGAAACACTTATGCTTATACAAATACAGATCATCT | 2220 |
| Db  | 2161 | CAAGTTTATCAGTAAATAAATCTGGAAAAACAGAAACACTTATGCTTATACAAATACAGATCATCT | 2220 |
| Qy  | 2221 | TGGAACCTGCATTTCTTCTGACACTGTTTATACACTGTGTAAATACCCATATGCTTGAAT       | 2280 |
| Db  | 2221 | TGGAACCTGCATTTCTTCTGACACTGTTTATACACTGTGTAAATACCCATATGCTTGAAT       | 2280 |
| Qy  | 2281 | TC 2282  |      |
| Db  | 2281 | TC 2282  |      |
| RESULT 4  |      |  |      |
| US-10-321-332-5   |      |  |      |
| ; Sequence 5, Application US/10321332                               |      |  |      |
| ; Publication No. US20030109677A1                                   |      |  |      |
| GENERAL INFORMATION:  |      |  |      |
| APPLICANT: Davis, et al.  |      |  |      |
| TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES THEREOF |      |  |      |
| NUMBER OF SEQUENCES: 6  |      |  |      |
| CORRESPONDENCE ADDRESS:   |      |  |      |
| ADDRESSEE: Regeneron Pharmaceuticals, Inc.                          |      |  |      |
| STREET: 777 Old Saw Mill River Road                                 |      |  |      |
| CITY: Tarrytown   |      |  |      |
| STATE: New York   |      |  |      |
| COUNTRY: USA  |      |  |      |
| ZIP: 10591  |      |  |      |
| COMPUTER READABLE FORM:   |      |  |      |
| MEDIUM TYPE: Floppy disk  |      |  |      |
| COMPUTER: IBM PC compatible   |      |  |      |
| OPERATING SYSTEM: PC-DOS/MS-DOS                                     |      |  |      |
| SOFTWARE: Patent In Release #1.0, Version #1.30                     |      |  |      |
| CURRENT APPLICATION DATA:   |      |  |      |
| APPLICATION NUMBER: US/10/321,332                                   |      |  |      |
| FILING DATE: 17-Dec-2002  |      |  |      |
| CLASSIFICATION: <Unknown>   |      |  |      |
| PRIOR APPLICATION DATA:   |      |  |      |
| APPLICATION NUMBER: US/08/373,579                                   |      |  |      |
| FILING DATE: 17-JAN-1995  |      |  |      |
| APPLICATION NUMBER: US 08/353,503                                   |      |  |      |
| FILING DATE: 09-DEC-1994  |      |  |      |
| APPLICATION NUMBER: US 08/348,492                                   |      |  |      |
| FILING DATE: 02-DEC-1994  |      |  |      |
| APPLICATION NUMBER: US 08/330,261                                   |      |  |      |
| FILING DATE: 27-OCT-1994  |      |  |      |
| APPLICATION NUMBER: US 08/319,932                                   |      |  |      |
| FILING DATE: 07-OCT-1994  |      |  |      |
| ATTORNEY/AGENT INFORMATION:   |      |  |      |
| NAME: Covert, Robert J.   |      |  |      |
| REGISTRATION NUMBER: REG 330-D                                      |      |  |      |
| TELECOMMUNICATION INFORMATION:                                      |      |  |      |
| TELEPHONE: (914) 345-7400   |      |  |      |
| TELEFAX: (914) 345-7721   |      |  |      |
| INFORMATION FOR SEQ ID NO: 5:                                       |      |  |      |
| SEQUENCE CHARACTERISTICS:   |      |  |      |
| LENGTH: 2282 base pairs   |      |  |      |
| TYPE: nucleic acid  |      |  |      |
| STRANDEDNESS: single  |      |  |      |
| TOPOLOGY: unknown   |      |  |      |
| MOLECULE TYPE: DNA (genomic)  |      |  |      |
| FEATURE:  |      |  |      |

|   |      |  |      |
|---|------|--|------|
| ; NAME/KEY: CDS   |      | US-10-321-332-5  |      |
| ; LOCATION: 357..1847   |      |  |      |
| ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:                         |      |  |      |
| Query Match 100.0%; Score 2282; DB 15; Length 2282;           |      |  |      |
| Best Local Similarity 100.0%; Pred. No. 0;                    |      |  |      |
| Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |      |  |      |
| QY  | 1    | GAATTCCTGGTGGTGGTATCTCTCCAGCCTTGAGGGAGGAAACAACACTGTAGGA        | 60   |
| DB  | 1    | GAATTCCTGGTGGTGGTATCTCTCCAGCCTTGAGGGAGGAAACAACACTGTAGGA        | 60   |
| QY  | 61   | TCTGGGAGAGAGAAACAAAGACCGTGAAGCTGCTCTGTAAAGCTGACACAGCCCTC       | 120  |
| DB  | 61   | TCTGGGAGAGAGAAACAAAGACCGTGAAGCTGCTCTGTAAAGCTGACACAGCCCTC       | 120  |
| QY  | 121  | CCAAGTGAGCAGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGATGCTGGAGAG      | 180  |
| DB  | 121  | CCAAGTGAGCAGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGATGCTGGAGAG      | 180  |
| QY  | 181  | AACACAGCAGTAAAAACAGGTTTGCTACTCGAAAAAGAGAAAGAGACTTTCATTG        | 240  |
| DB  | 181  | AACACAGCAGTAAAAACAGGTTTGCTACTCGAAAAAGAGAAAGAGACTTTCATTG        | 240  |
| QY  | 241  | ACGGACCCAGCCATGGCAGCGTAGCAGCCCTGCGTTTCAGACGGCAGCAGCTCGGGACTC   | 300  |
| DB  | 241  | ACGGACCCAGCCATGGCAGCGTAGCAGCCCTGCGTTTCAGACGGCAGCAGCTCGGGACTC   | 300  |
| QY  | 301  | TGGAAGTGTTTGGCCTCAAGTTTGTCTGAAGCTGCTCGTTTATTACTGAAGAAAGATGT    | 360  |
| DB  | 301  | TGGAAGTGTTTGGCCTCAAGTTTGTCTGAAGCTGCTCGTTTATTACTGAAGAAAGATGT    | 360  |
| QY  | 361  | GGCAGATTGTTTCTTACTCTGAGCTGTGATCTTGTCTGGCCGAGCCTATAACAACCT      | 420  |
| DB  | 361  | GGCAGATTGTTTCTTACTCTGAGCTGTGATCTTGTCTGGCCGAGCCTATAACAACCT      | 420  |
| QY  | 421  | TTTCGGAAGAGCATGGACAGCATAGGAAAGAAACAATATCAGGTCCAGCATGGTCTTGCA   | 480  |
| DB  | 421  | TTTCGGAAGAGCATGGACAGCATAGGAAAGAAACAATATCAGGTCCAGCATGGTCTTGCA   | 480  |
| QY  | 481  | GCTACACTTTCCTCTCCAGAGATGGACAACTGGCGCTCTTCTCCAGCCCTCAGTGT       | 540  |
| DB  | 481  | GCTACACTTTCCTCTCCAGAGATGGACAACTGGCGCTCTTCTCCAGCCCTCAGTGT       | 540  |
| QY  | 541  | CCAATGCTGTGACAGGACGCGCGCTCGAATACGATGACTCGGTGACAGGCTGCAAG       | 600  |
| DB  | 541  | CCAATGCTGTGACAGGACGCGCGCTCGAATACGATGACTCGGTGACAGGCTGCAAG       | 600  |
| QY  | 601  | TGCTGGAGAAATCATGGAAAAACAACACTCAGTGGCTAATGAAGCTTGAGAAATTATATCC  | 660  |
| DB  | 601  | TGCTGGAGAAATCATGGAAAAACAACACTCAGTGGCTAATGAAGCTTGAGAAATTATATCC  | 660  |
| QY  | 661  | AGGACAAATGAGAAAGAAATGGTAGATACAGCAGAAATGCAAGTACAGAACCCAGCG      | 720  |
| DB  | 661  | AGGACAAATGAGAAAGAAATGGTAGATACAGCAGAAATGCAAGTACAGAACCCAGCG      | 720  |
| QY  | 721  | CTGTGATGATAGAAATAGGGAACAACTCTGTGTGAACCAACAGCTGAGCAACCGGAAGT    | 780  |
| DB  | 721  | CTGTGATGATAGAAATAGGGAACAACTCTGTGTGAACCAACAGCTGAGCAACCGGAAGT    | 780  |
| QY  | 781  | TAACTGATGTGGAAGCCCAAGTATTAAATCAGACCACGAGCTTGAACCTTCAGCTCTTGG   | 840  |
| DB  | 781  | TAACTGATGTGGAAGCCCAAGTATTAAATCAGACCACGAGCTTGAACCTTCAGCTCTTGG   | 840  |
| QY  | 841  | TAACCTCCCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCAAGCCAGTGAATAA   | 900  |
| DB  | 841  | TAACCTCCCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCAAGCCAGTGAATAA   | 900  |
| QY  | 901  | ACAAATTGCAAGATGAAGAACAGTTTCTTGAAGAAAGAGGTGTAGCTATGGNAGCAAGC    | 960  |
| DB  | 901  | ACAAATTGCAAGATGAAGAACAGTTTCTTGAAGAAAGAGAGGTGTAGCTATGGNAGCAAGC  | 960  |
| QY  | 961  | ACATCATCCAACTACAGTCAATAAAGAGAAAGATCAGCTACAGGTGTTAGTATCCA       | 1020 |
| DB  | 961  | ACATCATCCAACTACAGTCAATAAAGAGAAAGATCAGCTACAGGTGTTAGTATCCA       | 1020 |
| QY  | 1021 | AGCAAAATTCATCATTTGAAGAACTAGAAAAAATAAGTAGTGCTGCCACGGTGAATAAT    | 1080 |
| DB  | 1021 | AGCAAAATTCATCATTTGAAGAACTAGAAAAAATAAGTAGTGCTGCCACGGTGAATAAT    | 1080 |
| QY  | 1081 | CAGTTCTTCAAAGCAGCAACATGATCTCATGGACAGCTTAATACTTACTGACTATGA      | 1140 |
| DB  | 1081 | CAGTTCTTCAAAGCAGCAACATGATCTCATGGACAGCTTAATACTTACTGACTATGA      | 1140 |
| QY  | 1141 | TGTCACACATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAGAAGAAACAATCAGCTTCA  | 1200 |
| DB  | 1141 | TGTCACACATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAGAAGAAACAATCAGCTTCA  | 1200 |
| QY  | 1201 | GAGACTGTGCTGAAGTATTCAAATCAGGACACACACAATAATGGCATCTACAGTTAAACAT  | 1260 |
| DB  | 1201 | GAGACTGTGCTGAAGTATTCAAATCAGGACACACACAATAATGGCATCTACAGTTAAACAT  | 1260 |
| QY  | 1261 | TCCCTTAATTTACAGAAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGAGCGGGT    | 1320 |
| DB  | 1261 | TCCCTTAATTTACAGAAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGAGCGGGT    | 1320 |
| QY  | 1321 | GGACAATTTATTCAGCGACGTGAGGATGCGAGCTTTTTCAGAGGACTTGGAAAGAAAT     | 1380 |
| DB  | 1321 | GGACAATTTATTCAGCGACGTGAGGATGCGAGCTTTTTCAGAGGACTTGGAAAGAAAT     | 1380 |
| QY  | 1381 | ATAAAGTGGATTTGGTAAACCTTCAGGAGAAATATTGGCTGGGAAATGAGTTTGTTCGC    | 1440 |
| DB  | 1381 | ATAAAGTGGATTTGGTAAACCTTCAGGAGAAATATTGGCTGGGAAATGAGTTTGTTCGC    | 1440 |
| QY  | 1441 | AACTGACTTAATCAGCAACGCTATGCTTAAATAACACTTAAAGACTGGGAAGGGAATG     | 1500 |
| DB  | 1441 | AACTGACTTAATCAGCAACGCTATGCTTAAATAACACTTAAAGACTGGGAAGGGAATG     | 1500 |
| QY  | 1501 | AGGCTTACTCATTTGATGAACAATTTCTATCTCTCAAGTGAAGAACTCAATTTATAGGATTC | 1560 |
| DB  | 1501 | AGGCTTACTCATTTGATGAACAATTTCTATCTCTCAAGTGAAGAACTCAATTTATAGGATTC | 1560 |
| QY  | 1561 | ACCTTAAAGGACTTACAGGACAGCCGCAAAATAAGCAGCATCAGCCAAACAGGAATG      | 1620 |
| DB  | 1561 | ACCTTAAAGGACTTACAGGACAGCCGCAAAATAAGCAGCATCAGCCAAACAGGAATG      | 1620 |
| QY  | 1621 | ATTTTAGCAAAAGATGGAGAACAGCAAAATGTTTGCATAAATGTTTCAAAATGCTTAA     | 1680 |
| DB  | 1621 | ATTTTAGCAAAAGATGGAGAACAGCAAAATGTTTGCATAAATGTTTCAAAATGCTTAA     | 1680 |
| QY  | 1681 | CAGGAGGCTGGTGGTTCATGATGCTTCCAACTTGAAACGGAATGTACTATCCAC         | 1740 |
| DB  | 1681 | CAGGAGGCTGGTGGTTCATGATGCTTCCAACTTGAAACGGAATGTACTATCCAC         | 1740 |
| QY  | 1741 | AGAGGAGAAACAATAAAGTTTCAACGGCAATTAATGTTTACTTCTGGAAGGCTCAGGCT    | 1800 |
| DB  | 1741 | AGAGGAGAAACAATAAAGTTTCAACGGCAATTAATGTTTACTTCTGGAAGGCTCAGGCT    | 1800 |
| QY  | 1801 | ATTTCTCTCAAGGCCAACACCATGATGATCGGACAGAGATTTCTAACAATCCAGTCCA     | 1860 |
| DB  | 1801 | ATTTCTCTCAAGGCCAACACCATGATGATCGGACAGAGATTTCTAACAATCCAGTCCA     | 1860 |
| QY  | 1861 | CCTGAGGAACTGTCTCGAACTATTTTCAAAGACTTAAAGCCAGTGCACTGAAAGTCAAG    | 1920 |
| DB  | 1861 | CCTGAGGAACTGTCTCGAACTATTTTCAAAGACTTAAAGCCAGTGCACTGAAAGTCAAG    | 1920 |
| QY  | 1921 | CTGGCAGCTGTGCTCTTCCACACAGAGGCGGTGCTCGGTGCTGACGGGACCCACA        | 1980 |
| DB  | 1921 | CTGGCAGCTGTGCTCTTCCACACAGAGGCGGTGCTCGGTGCTGACGGGACCCACA        | 1980 |
| QY  | 1981 | TGCTCCAGATTAGAGCCTGTAACTTTTATCACTTAACTTGCATCACTTAAACGACCAA     | 2040 |
| DB  | 1981 | TGCTCCAGATTAGAGCCTGTAACTTTTATCACTTAACTTGCATCACTTAAACGACCAA     | 2040 |
| QY  | 2041 | GCAAGACCTTAAACATCCATTAATTGTGATTAGACAGAAACCTTATGCAAGATGAACCG    | 2100 |



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Db 1441 AACTGACTAATCAGCAACCTATGTCTTAAATAACCTTAAAGACTGGGAAGGAATG 1500
Qy 1501 AGGCTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTATAGGATTC 1560
Db 1501 AGGCTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTATAGGATTC 1560
Qy 1561 ACCTTAAAGGACTTACAGGACAGCGGCAAAATAGAGCAGTCAGCCACAGGAAATG 1620
Db 1561 ACCTTAAAGGACTTACAGGACAGCGGCAAAATAGAGCAGTCAGCCACAGGAAATG 1620
Qy 1621 ATTTTAGCAAAAGATGAGACACAGCAAAATGATTTGCAAAATGTTTCAAAATGCTTAA 1680
Db 1621 ATTTTAGCAAAAGATGAGACACAGCAAAATGATTTGCAAAATGTTTCAAAATGCTTAA 1680
Qy 1681 CAGGAGGCTGGTGGTGTGATGATGTCCTTCCAACTTGAACGGAATGTACTATCCAC 1740
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Qy 1741 AGAGGAGAAACAATAAGTTCAACGGCAATTAATGTGTACTAGGAAAGGCTCAGGCT 1800
Db 1741 AGAGGAGAAACAATAAGTTCAACGGCAATTAATGTGTACTAGGAAAGGCTCAGGCT 1800
Qy 1801 ATTCGCTCAAGGCCACAAACCATGATCCGACCGAGATTTCTTAAACATCCAGTCCA 1860
Db 1801 ATTCGCTCAAGGCCACAAACCATGATCCGACCGAGATTTCTTAAACATCCAGTCCA 1860
Qy 1861 CCTGAGGAACTGCTCGAACTATTTTCAAGAACTTAAAGCCAGTGCACTGAAAGTCACGG 1920
Db 1861 CCTGAGGAACTGCTCGAACTATTTTCAAGAACTTAAAGCCAGTGCACTGAAAGTCACGG 1920
Qy 1921 CTGCGCACTGTGCTCTTCCACCAAGAGGCGGTGCTCGGTGCTGACGGGACCCACA 1980
Db 1921 CTGCGCACTGTGCTCTTCCACCAAGAGGCGGTGCTCGGTGCTGACGGGACCCACA 1980
Qy 1981 TGCTCCAGATTAGCGCTTAACTTTATCACTTAACTTAACTTAACTTAACTTAACTTAA 2040
Db 1981 TGCTCCAGATTAGCGCTTAACTTTATCACTTAACTTAACTTAACTTAACTTAACTTAA 2040
Qy 2041 GCAAGACCTTAAACATCCATATTTGATTAGACAGAAACACCTATGCAAGGATGAACCG 2100
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Db 2161 CAAAGTTTATCAGTAAATAACTGGAACACAGACACTTATGTTATACAAATACAGATCATCT 2220
Qy 2221 TGGAACTGCATTTCTTGAGCACTGTTTATACACTGTGTAAATACCCATATGCTCGTAAT 2280
Db 2221 TGGAACTGCATTTCTTGAGCACTGTTTATACACTGTGTAAATACCCATATGCTCGTAAT 2280
Qy 2281 TC 2282
Db 2281 TC 2282
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RESULT 6
US-10-179-820-5
; Sequence 5, Application US/10179820
; Publication No. US20030166858A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel et al.
; TITLE OF INVENTION: TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF
; FILE REFERENCE: REG 330-F-PCT-US
; CURRENT APPLICATION NUMBER: US/10179,820
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US/08/817,318
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 6
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; SOFTWARE: FastSBQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: CDS
; LOCATION: (357)...(1847)
US-10-179-820-5
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Query Match 100.0%; Score 2282; DB 16; Length 2282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 TCTGGGAGAGAGGAACAAGGACCGTGAAGCTCTCTGTAAAAAGCTGACACAGCCCTC 120
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Db 121 CCAAGTGAGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGCGAGAG 180
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Qy 361 GGCAGATTGTTTCTTTTACTCTGAGCTGTGATCTTTGCTGGCCGAGCTATAACAAT 420
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Qy 421 TTCCGAAAGAGCATGACAGCATAGGAAAGAAATATCAGGTCCAGCATGGGTCTGCA 480
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Qy 481 GGTACACTTCTCTCCAGAGATGGACAACTGCGCTCTTCTCCAGCCCTTAGGTGT 540
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Qy 541 CCAATGCTGTGAGAGGACCGCCGCTCGAATACGATGACTCGGTGAGAGGCTGCAAG 600
Db 541 CCAATGCTGTGAGAGGACCGCCGCTCGAATACGATGACTCGGTGAGAGGCTGCAAG 600
Qy 601 TGCTGGAGAACATCATGGAAGAAACAACACTCAGTGGCTTAATGAAGCTTGAGAAATTATCC 660
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Qy 661 AGGACAAATGAGAAAGAAATGTAGAGATACAGCAATGCAGTACAGAACCCAGACGG 720
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Qy 721 CTGTGATGATGAAATAGGCAAAACCTTGTGAAACCAACAGCTGAGCAAAACCGGAAGT 780
Db 721 CTGTGATGATGAAATAGGCAAAACCTTGTGAAACCAACAGCTGAGCAAAACCGGAAGT 780
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Db 841 ||||| AACACTCCCTCTGCAAAACAAATTGGAATAA 900  
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Db 2161 CAAAGTTTATCAGTAAATAAATCTGAAAAAGAGAACTTATGTTATACATCAGATCATCT 2220  
Qy 2221 TGGAACTGATTTCTTCTGAGCACTGTTTATACACTGTGTAATACCATATGCTCTGAAT 2280  
Db 2221 TGGAACTGATTTCTTCTGAGCACTGTTTATACACTGTGTAATACCATATGCTCTGAAT 2280  
Qy 2281 TC 2282  
Db 2281 TC 2282

RESULT 7  
US-10-603-293-5  
; Sequence 5, Application US/10603293  
; Publication No. US20050100906A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Samuel et al.  
; TITLE OF INVENTION: Tie-2 Ligands, Methods of Making and Uses Thereof  
; FILE REFERENCE: REG 330-G-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/603,293  
; CURRENT FILING DATE: 2003-06-25  
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/08/930,721  
; PRIOR FILING DATE: FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT/US96/04806  
; PRIOR FILING DATE: FILING DATE: 1996-04-05  
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT/US95/12935  
; PRIOR FILING DATE: FILING DATE: 1995-10-06  
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 08/418,595  
; PRIOR FILING DATE: FILING DATE: 1996-04-05  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 2282  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (357)..(1844)  
US-10-603-293-5

Query Match 100.0%; Score 2282; DB 21; Length 2282;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCCTGGGTTGGTGGTTTATCTCTCCAGCCCTTGGAGGGAGGAAACACACTGTAGGA 60  
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Qy 61 TCTGGGAGAGAGAGAAACAAAGGACCGTGAAGCTGCTGTGTAAGCTGACACAGCCCTC 120  
Db 61 TCTGGGAGAGAGAGAAACAAAGGACCGTGAAGCTGCTGTGTAAGCTGACACAGCCCTC 120  
Qy 121 CCAAGTGAAGAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGCTGAGAG 180  
Db 121 CCAAGTGAAGAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGCTGAGAG 180  
Qy 181 AACACAGCAGTAAACACCAAGGTTTGCTACTGGAAAAAGAGAGAAAGACTTTCATTG 240



181 AACACAGCAGTAAACCCAGGTTTGCTACTGGAAGAGGAGAGAAAGACTTTTCATTG 240  
241 ACGGACCCAGCCATGGCAGCGTAGCAGCCCTCGGTTTTCAGAGCGCAGCAGCTCGGGACTC 300  
241 ACGGACCCAGCCATGGCAGCGTAGCAGCCCTCGGTTTTCAGAGCGCAGCAGCTCGGGACTC 300  
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301 TGGACGTGTGTTGCCCTCAAGTTTGCTAAGCTGCTGGTTTATTACTGAAGAAAGAAATGT 360  
361 GGCAGATTCTTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCCCTATACAACT 420  
361 GGCAGATTCTTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCCCTATACAACT 420  
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481 GTTACACTTTCTCTCTGCGAGATGGACAACTGCGGCTCTTCTCCAGCCCTACGTGT 540  
481 GCTACACTTTCTCTCTGCGAGATGGACAACTGCGGCTCTTCTCCAGCCCTACGTGT 540  
541 CCAATGCTGTGAGAGGAGCGCGCTCGAATACGATGCACTCGGTGCGAGGGCTGCAAG 600  
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601 TGCCTGAGAAACATCATGGAAAAACAACACTCAGTGGCTAATGAAGCTTGAGAAATTATATCC 660  
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721 CTGTGATGATAGAAATAGGACCAACCTGTTGAAACCAACAGCTCAGCAACCGCGGAGT 780  
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781 TAACTGATGTGAAGCCCAAGTATTAAATCAGACCAAGACTTGAACCTTCAGCTCTTGG 840  
841 AACACTCCCTCTCGACAAACAAATTTGGAAAAACAGATTTGGACCAAGACAGCTGGAATAA 900  
841 AACACTCCCTCTCGACAAACAAATTTGGAAAAACAGATTTGGACCAAGACAGCTGGAATAA 900  
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1201 GAGACTGTGCTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTACAGTTAAACAT 1260  
1261 TCCCTAAATTCTACAGAGAGATCAAGGCCCTACTGTGACATGGAAGCTGAGGAGCGGGT 1320

1261 TCCCTAAATTCTACAGAGAGATCAAGGCCCTACTGTGACATGGAAGCTGAGAGAGCGGGT 1320  
1321 GGACAAATTTATTCAGCGACGTGAGGATGCGAGCGTTGATTTTTCAGAGGACTTCGGAAGRAAT 1380  
1321 GGACAAATTTATTCAGCGACGTGAGGATGCGAGCGTTGATTTTTCAGAGGACTTCGGAAGRAAT 1380  
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1621 ATTTTAGCACAAAGGATGAGACACGACAAATGATTTTGCAAAATGTTTACAAATGCTTAA 1680  
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1741 AGAGCAGAAACAAATAAAGTTCAACGGCANTTAATGCTACTCTGGAAGAGCTCAGGCT 1800  
1741 AGAGCAGAAACAAATAAAGTTCAACGGCANTTAATGCTACTCTGGAAGAGCTCAGGCT 1800  
1801 ATTCCTCTCAAGGCCAACACCATGATGATCCGACAGCAGATTTCTTAAACATCCAGTCCA 1860  
1801 ATTCCTCTCAAGGCCAACACCATGATGATCCGACAGCAGATTTCTTAAACATCCAGTCCA 1860  
1861 CTTGAGGAACCTGTCTCGAACTATTCTTCAAGACTTAAAGCCAGTGCTGAAAGTCAAG 1920  
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1921 CTGGCAGCTGTCTCTTCCACACAGAGGGCGTGTCTCGGTCTGACGGGACCCACA 1980  
1921 CTGGCAGCTGTCTCTTCCACACAGAGGGCGTGTCTCGGTCTGACGGGACCCACA 1980  
1981 TGCTCCAGATTAGAGCCCTGTAAAATTTTATCACTTAAACTTGCATCACTTAAACGACCAA 2040  
1981 TGCTCCAGATTAGAGCCCTGTAAAATTTTATCACTTAAACTTGCATCACTTAAACGACCAA 2040  
2041 GCAAGACCTTAAACATCCATTAATTTGTGATTAGACAGAAACACCTATGCAAGATGAACCG 2100  
2041 GCAAGACCTTAAACATCCATTAATTTGTGATTAGACAGAAACACCTATGCAAGATGAACCG 2100  
2101 AGGCTGAGAAATCAGACTGACAGTGTTCAGAGCGTGTCTGCTCAACCAAGATGTTATGTG 2160  
2101 AGGCTGAGAAATCAGACTGACAGTGTTCAGAGCGTGTCTGCTCAACCAAGATGTTATGTG 2160  
2161 CAAAGTTTATCAGTAAATAACTTGAAGAAACAGAAACACTTATGTTTATAAATAACAGATCACT 2220  
2161 CAAAGTTTATCAGTAAATAACTTGAAGAAACAGAAACACTTATGTTTATAAATAACAGATCACT 2220  
2221 TGGAACTGCAATCTTCTGAGCAGCTGTTTATACACTGTGTAAATACCCATATGCTCTGAAT 2280  
2221 TGGAACTGCAATCTTCTGAGCAGCTGTTTATACACTGTGTAAATACCCATATGCTCTGAAT 2280  
2281 TC 2282  
2281 TC 2282





Db 1741 AGAGGAGAAACAAATAAGTTCAACGGCAATTAATAGTGTACTACTGGAAAGGCTCAGGCT 1800  
QY 1801 ATTTCGCTCAAGGCCCAACCATGATCCGACACGAGAGATTTCTAAACATCCCAAGTCCA 1860  
Db 1801 ATTTCGCTCAAGGCCCAACCATGATCCGACACGAGATTTCTAAACATCCCAAGTCCA 1860  
QY 1861 CTTGAGGAATCTGTCTGAACTATTTTCAAGACTTTAAAGCCAGTGCACCTGAAAGTCAAGG 1920  
Db 1861 CTTGAGGAATCTGTCTGAACTATTTTCAAGACTTTAAAGCCAGTGCACCTGAAAGTCAAGG 1920  
QY 1921 CTGCGGCACTGTCTCTTCCACACAGAGGGCGGTGTCTCGGTGTGACGGGACCCACA 1980  
Db 1921 CTGCGGCACTGTCTCTTCCACACAGAGGGCGGTGTCTCGGTGTGACGGGACCCACA 1980  
QY 1981 TGCTCCAGATTAGAGCTGTAAACTTTATCACTTAAACTTTGCATCACTTAAACGCGACCAA 2040  
Db 1981 TGCTCCAGATTAGAGCTGTAAACTTTATCACTTAAACTTTGCATCACTTAAACGCGACCAA 2040  
QY 2041 GCAAGACCCCTAAACATCCATAATTGTGATTAGACAGAACACCTATGCAAGATGAACCCG 2100  
Db 2041 GCAAGACCCCTAAACATCCATAATTGTGATTAGACAGAACACCTATGCAAGATGAACCCG 2100  
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Db 2161 CAAAGTTTATCAGTAAATAACTGGAACACAGAACACTTATGTTATACAAATACAGATCATCT 2220  
QY 2221 TCGAACTGCATTTCTTGAGCACTGTTTATACACTGTGTGAAATACCCATATGCTCTGAAT 2280  
Db 2221 TCGAACTGCATTTCTTGAGCACTGTTTATACACTGTGTGAAATACCCATATGCTCTGAAT 2280  
QY 2281 TC 2282  
Db 2281 TC 2282

RESULT 9  
US-09-998-831-3  
; Sequence 3, Application US/09998831  
; Patent No. US20020119153A1  
; GENERAL INFORMATION:  
; APPLICANT: Philip E. Thorpe  
; APPLICANT: Rolf A. Breken  
; TITLE OF INVENTION: ANTI-BODY CONJUGATE COMPOSITIONS FOR SELECTIVELY  
; TITLE OF INVENTION: INHIBITING VEGF  
; FILE REFERENCE: 4001.002584  
; CURRENT APPLICATION NUMBER: US/09/998,831  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 09/561,108  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 2269  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-998-831-3

Query Match 99.4%; Score 2269; DB 9; Length 2269;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 TGGGTGTGTTTATCTCTCCAGCCTTGGAGGGGAAACAACCTGTAGATCTGGGG 60  
QY 68 AGAGAGGACAAAGACCGTGAAGCTGCTGTAAAGCTGACACGACCCCTCCCAAGTG 127  
Db 61 AGAGAGGACAAAGACCGTGAAGCTGCTGTAAAGCTGACACGACCCCTCCCAAGTG 120

QY 128 AGCAGGACTGTTCTTTCCCACTGCAATCTGACAGTTTACTGCAATGCTCTGAGAGAACACAG 187  
Db 121 AGCAGGACTGTTCTTTCCCACTGCAATCTGACAGTTTACTGCAATGCTCTGAGAGAACACAG 180  
QY 188 CAGTAAAAACCAAGTTTGTCTACTGAAAAAGAGGAGAGAGACTTTTCATTTGACGGACC 247  
Db 181 CAGTAAAAACCAAGTTTGTCTACTGAAAAAGAGGAGAGAGACTTTTCATTTGACGGACC 240  
QY 248 CAGCCATAGCAGCTAGCAGCCCTGCTTTTCAGACGGCAGCAGCTCGGACCTCTGGACCT 307  
Db 241 CAGCCATAGCAGCTAGCAGCCCTGCTTTTCAGACGGCAGCAGCTCGGACCTCTGGACCT 300  
QY 308 GTGTTTGCCTCAAGTTTGTCTAAGCTGTCTGTTTATTACTGAAGAAAGAAATGTGCAGAT 367  
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QY 368 TGTTTTCTTACTCTGAGCTGTGATCTTGTCTTGGCCGCGAGCTATATAACAATTTTCGGA 427  
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QY 428 GAGCATGACAGCATAGGAAAGAACATATCAGGTCCAGCATGGGTCTCTGAGCTTACAC 487  
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QY 608 GAAACATCATGGAACAAACACACTCAGTGGCTAATGAAGCTTGAGAAATTTATCCAGGACAA 667  
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QY 968 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTTACAGGTGTGTAGTATCCAAAGCAAA 1027  
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Db 1081 TCAAAAGCAGCAATGATCTCATGAGACAGTTTAACTTAACTTACTGATGATGTCCAC 1140  
QY 1148 ATCAAACCTCAGCTAAGGACCCCACTGTTGTCTTAAAGAGAAACAAATCAGCTTTCAGAGACTG 1207  
Db 1141 ATCAAACCTCAGCTAAGGACCCCACTGTTGTCTTAAAGAGAAACAAATCAGCTTTCAGAGACTG 1200  
QY 1208 TGCTGAAGTATTTCAAATCAGGACACACCAACAAATGGCATCTTACAGTTTAAACATTCCTTAA 1267

|    |      |  |  |      |
|----|------|--|--|------|
| Db | 1201 |  | TGCTGAAGTATTCAATATCAGGACACACCACAAATGGCATCTACAGTAACTCCCTAA      | 1260 |
| Qy | 1268 |  | TTCTACAGAGAGATCAAGSCCTACTGTGATGGAAGCTGGAGGAGGGGTGGCAAT         | 1327 |
| Db | 1261 |  | TTCTACAGAGAGATCAAGSCCTACTGTGATGGAAGCTGGAGGAGGGGTGGCAAT         | 1320 |
| Qy | 1328 |  | TATTCAGCGACGTGAGGATGGCAGCGTTGATTTTCAGAGACTTGAAGAATATATAAGT     | 1387 |
| Db | 1321 |  | TATTCAGCGACGTGAGGATGGCAGCGTTGATTTTCAGAGACTTGAAGAATATATAAGT     | 1380 |
| Qy | 1388 |  | GGGATTTGGTAAACCTTCAGGAGAAATATGGCTGGGAAATGAGTTTTCGCAACTGAC      | 1447 |
| Db | 1381 |  | GGGATTTGGTAAACCTTCAGGAGAAATATGGCTGGGAAATGAGTTTTCGCAACTGAC      | 1440 |
| Qy | 1448 |  | TAATCAGCAACGCTATGTGCTTAAATAACACCTTAAAGACTGGGAAGGGAATGAGGCTTA   | 1507 |
| Db | 1441 |  | TAATCAGCAACGCTATGTGCTTAAATAACACCTTAAAGACTGGGAAGGGAATGAGGCTTA   | 1500 |
| Qy | 1508 |  | CTCATTTGATGAACATTTCTATCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA    | 1567 |
| Db | 1501 |  | CTCATTTGATGAACATTTCTATCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA    | 1560 |
| Qy | 1568 |  | AGGACTTACAGGACAGCCGGCAAAATAGCAGCATCAGCAACCCAGGAAATGATTTAG      | 1627 |
| Db | 1561 |  | AGGACTTACAGGACAGCCGGCAAAATAGCAGCATCAGCAACCCAGGAAATGATTTAG      | 1620 |
| Qy | 1628 |  | CACAAAGGATGGAGAACACCAAAATGATTTTCAATGTTTCAAAATGCTTAACAGAGG      | 1687 |
| Db | 1621 |  | CACAAAGGATGGAGAACACCAAAATGATTTTCAATGTTTCAAAATGCTTAACAGAGG      | 1680 |
| Qy | 1688 |  | CTGGTGGTTTGATGATGCTGCTTCCAACTTGAACGGAAATGATCTATCCACAGAGGCA     | 1747 |
| Db | 1681 |  | CTGGTGGTTTGATGATGCTGCTTCCAACTTGAACGGAAATGATCTATCCACAGAGGCA     | 1740 |
| Qy | 1748 |  | GAAACACAAATPAAGTTCAACGGCAATTAATGGTACTACTGAAAGGCTCAGGCTATTCGCT  | 1807 |
| Db | 1741 |  | GAAACACAAATPAAGTTCAACGGCAATTAATGGTACTACTGAAAGGCTCAGGCTATTCGCT  | 1800 |
| Qy | 1808 |  | CAAGGCCACAAACCATGATGATCGACAGGAGATTTCTAAACATCCAGTCCACCTGAGG     | 1867 |
| Db | 1801 |  | CAAGGCCACAAACCATGATGATCGACAGGAGATTTCTAAACATCCAGTCCACCTGAGG     | 1860 |
| Qy | 1868 |  | AACGTCTCGAACTATTTTCAAGACTTAAGCCAGTGCATGAAAGTCAAGGCTGCGCA       | 1927 |
| Db | 1861 |  | AACGTCTCGAACTATTTTCAAGACTTAAGCCAGTGCATGAAAGTCAAGGCTGCGCA       | 1920 |
| Qy | 1928 |  | CTGTGCTCTCTTCCACACAGAGGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA    | 1987 |
| Db | 1921 |  | CTGTGCTCTCTTCCACACAGAGGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA    | 1980 |
| Qy | 1988 |  | GATTAGAGCCTGTAACCTTTATCACTTAAACTTGCATCACTTAACGACCAACAGCAGAC    | 2047 |
| Db | 1981 |  | GATTAGAGCCTGTAACCTTTATCACTTAAACTTGCATCACTTAACGACCAACAGCAGAC    | 2040 |
| Qy | 2048 |  | CCTAAACATCCATAATTTGATATTAGACAGAACACTATGCAAGATGAAACCCGAGGCTGA   | 2107 |
| Db | 2041 |  | CCTAAACATCCATAATTTGATATTAGACAGAACACTATGCAAGATGAAACCCGAGGCTGA   | 2100 |
| Qy | 2108 |  | GAATCAGACTGACAGTTTACAGAGCGTGTGCTGTCACAAACCAAGATGTTATGTGCAAGTTT | 2167 |
| Db | 2101 |  | GAATCAGACTGACAGTTTACAGAGCGTGTGCTGTCACAAACCAAGATGTTATGTGCAAGTTT | 2160 |
| Qy | 2168 |  | ATCAGTAAATTAACCTGGAAAAACAGAACTTATGTTTATACATATCAGATCATCTTGGAACT | 2227 |
| Db | 2161 |  | ATCAGTAAATTAACCTGGAAAAACAGAACTTATGTTTATACATATCAGATCATCTTGGAACT | 2220 |
| Qy | 2228 |  | GCATTTCTGAGCAGCTTTTATACATGTTGTAATACCCATATGCTCT                 | 2276 |
| Db | 2221 |  | GCATTTCTGAGCAGCTTTTATACATGTTGTAATACCCATATGCTCT                 | 2269 |

|  |     |             |   |     |  |  |  |  |  |
|--|-----|-------------|---|-----|--|--|--|--|--|
| US-09-998-833-3  |     |             |   |     |  |  |  |  |  |
| ; Sequence 3, Application US/09998833                              |     |             |   |     |  |  |  |  |  |
| ; Publication No. US20030082187A1                                  |     |             |   |     |  |  |  |  |  |
| ; GENERAL INFORMATION:   |     |             |   |     |  |  |  |  |  |
| ; APPLICANT: THORPE, PHILIP E.                                     |     |             |   |     |  |  |  |  |  |
| ; APPLICANT: RAN, SOPHIA   |     |             |   |     |  |  |  |  |  |
| ; TITLE OF INVENTION: CANCER TREATMENT METHODS USING ANTIBODIES TO |     |             |   |     |  |  |  |  |  |
| ; TITLE OF INVENTION: AMINOPHOSPHOLIPIDS                           |     |             |   |     |  |  |  |  |  |
| ; FILE REFERENCE: 4001.002200                                      |     |             |   |     |  |  |  |  |  |
| ; CURRENT APPLICATION NUMBER: US/09/998,833                        |     |             |   |     |  |  |  |  |  |
| ; CURRENT FILING DATE: 2001-11-30                                  |     |             |   |     |  |  |  |  |  |
| ; PRIOR APPLICATION NUMBER: US/09/351,543                          |     |             |   |     |  |  |  |  |  |
| ; PRIOR FILING DATE: 1999-07-12                                    |     |             |   |     |  |  |  |  |  |
| ; NUMBER OF SEQ ID NOS: 5  |     |             |   |     |  |  |  |  |  |
| ; SOFTWARE: PatentIn Ver. 2.0                                      |     |             |   |     |  |  |  |  |  |
| ; SEQ ID NO 3  |     |             |   |     |  |  |  |  |  |
| ; LENGTH: 2269   |     |             |   |     |  |  |  |  |  |
| ; TYPE: DNA  |     |             |   |     |  |  |  |  |  |
| ; ORGANISM: Homo sapiens   |     |             |   |     |  |  |  |  |  |
| US-09-998-833-3  |     |             |   |     |  |  |  |  |  |
| Query Match 99.4%; Score 2269; DB 10; Length 2269;                 |     |             |   |     |  |  |  |  |  |
| Best Local Similarity 100.0%; Pred. No. 0;                         |     |             |   |     |  |  |  |  |  |
| Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;      |     |             |   |     |  |  |  |  |  |
| Qy   | 8   | TGGTGTGGTGT | TATCTCTCCAGCGCTTGAGGGAGGGAACAACACTGTAGGATCTGGGG         | 67  |  |  |  |  |  |
| Db   | 1   | TGGTGTGGTGT | TATCTCTCCAGCGCTTGAGGGAGGGAACAACACTGTAGGATCTGGGG         | 60  |  |  |  |  |  |
| Qy   | 68  | AGAGAGAA    | CAAAGNACCTGAAAGCTGCTCTGTAAGAGCTGACACAGCCCTCCCAAGTG      | 127 |  |  |  |  |  |
| Db   | 61  | AGAGAGAA    | CAAAGGACCGTGAAGTGTCTGTAAAGCTGACACAGCCCTCCCAAGTG         | 120 |  |  |  |  |  |
| Qy   | 128 | AGCAGACTGT  | TCTTCCCACTGCAATCTGACAGTCTTACTGCATGCTCTGGAGAGAACACAG     | 187 |  |  |  |  |  |
| Db   | 121 | AGCAGACTGT  | TCTTCCCACTGCAATCTGACAGTCTTACTGCATGCTCTGGAGAGAACACAG     | 180 |  |  |  |  |  |
| Qy   | 188 | CAGTAAAA    | ACAGGTTTGTCTTGGAAAAAGAGAGAAAGAGAGACTTTTCATTTGACGACC     | 247 |  |  |  |  |  |
| Db   | 181 | CAGTAAAA    | ACCAAGTTTGTCTTGGAAAAAGAGAGAAAGAGAGACTTTTCATTTGACGACC    | 240 |  |  |  |  |  |
| Qy   | 248 | CAGCCATG    | CAGCGTAGCAGCCCTCGTTTTCAGACGCGCAGCTCGGGACTCTGGACGT       | 307 |  |  |  |  |  |
| Db   | 241 | CAGCCATG    | CAGCGTAGCAGCCCTCGGTTTTCAGACGCGCAGCTCGGGACTCTGGACGT      | 300 |  |  |  |  |  |
| Qy   | 308 | GTGTTTGC    | CCCTCAAGTTTGTCTAAGCTGCTGTTTATTTACTGAAGAAAGAAATGTGGCAGAT | 367 |  |  |  |  |  |
| Db   | 301 | GTGTTTGC    | CCCTCAAGTTTGTCTAAGCTGCTGTTTATTTACTGAAGAAAGAAATGTGGCAGAT | 360 |  |  |  |  |  |
| Qy   | 368 | TGTTTCTTT   | TACTCTGAGCTGTGATCTTGTCTTGGCGCGCAGCTTATAACAACTTTTCGGAA   | 427 |  |  |  |  |  |
| Db   | 361 | TGTTTCTTT   | TACTCTGAGCTGTGATCTTGTCTTGGCGCGCAGCTTATAACAACTTTTCGGAA   | 420 |  |  |  |  |  |
| Qy   | 428 | GAGCATGG    | CAGCATAGGAAAGAGCAATATCAGGTCAGATCGGTCCAGTGGTCTGACGCTACAC | 487 |  |  |  |  |  |
| Db   | 421 | GAGCATGG    | CAGCATAGGAAAGAGCAATATCAGGTCAGATCGGTCCAGTGGTCTGACGCTACAC | 480 |  |  |  |  |  |
| Qy   | 488 | TTTCTCTCT   | GCCAGAGATGGACAACCTGCCGCTCTTCTCCAGCCCTTACGTGTCCAATGC     | 547 |  |  |  |  |  |
| Db   | 481 | TTTCTCTCT   | GCCAGAGATGGACAACCTGCCGCTCTTCTCCAGCCCTTACGTGTCCAATGC     | 540 |  |  |  |  |  |
| Qy   | 548 | TGTGCGAG    | GAGGAGCGCGCGCTCGAATACGATGACTCGGTGCGAGGCTGCAAGTGTCTGGA   | 607 |  |  |  |  |  |
| Db   | 541 | TGTGCGAG    | GAGGAGCGCGCGCTCGAATACGATGACTCGGTGCGAGGCTGCAAGTGTCTGGA   | 600 |  |  |  |  |  |
| Qy   | 608 | GAAATCAT    | TGAGAAACAACTCAGTGGCTTAATGAAGCTTGAGATTTATATCCAGGACAA     | 667 |  |  |  |  |  |
| Db   | 601 | GAAATCAT    | TGAGAAACAACTCAGTGGCTTAATGAAGCTTGAGATTTATATCCAGGACAA     | 660 |  |  |  |  |  |
| Qy   | 668 | CATGAAGA    | AGAAATGCTAGAGATACAGCAGAAATGACAGAACACAGCGGCTGTGAT        | 727 |  |  |  |  |  |
| Db   | 661 | CATGAAGA    | AGAAATGCTAGAGATACAGCAGAAATGACAGAACACAGCGGCTGTGAT        | 720 |  |  |  |  |  |

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QY 728 GATAGAAATAGGACAAACCTGTTGAACCAAAACAGCTGAGCAAAACCGGAAAGTTAACTGA 787
Db 721 GATAGAAATAGGACAAACCTGTTGAACCAAAACAGCTGAGCAAAACCGGAAAGTTAACTGA 780
QY 788 TGTGGAAGCCCAAGTATTAAATCAGACCAAGAGACTTGAACCTTCACTCTTGGACACATC 847
Db 781 TGTGGAAGCCCAAGTATTAAATCAGACCAAGAGACTTGAACCTTCACTCTTGGACACATC 840
QY 848 CCTCTCGACAAACAAATTTGGAATAAAGACAGATTTGGACCAAGACAGCTGAAATATAAACAAT 907
Db 841 CCTCTCGACAAACAAATTTGGAATAAAGACAGATTTGGACCAAGACAGCTGAAATATAAACAAT 900
QY 908 GCAAGATTAAGACAGTTTCTTAGAAGAAAGGTGCTAGCTATGGAAGACAAGCAATCAT 967
Db 901 GCAAGATTAAGACAGTTTCTTAGAAGAAAGGTGCTAGCTATGGAAGACAAGCAATCAT 960
QY 968 CCAACTACAGTCAATAAAGAAAGAGAGATCAGCTACAGGTGTAGTATCCAAGCAAAA 1027
Db 961 CCAACTACAGTCAATAAAGAAAGAGAGATCAGCTACAGGTGTAGTATCCAAGCAAAA 1020
QY 1028 TTCCATCATTGAAGAACTAGAAAAAAAATAGTACTGCCACGGTGAATAATTCAGTTCT 1087
Db 1021 TTCCATCATTGAAGAACTAGAAAAAAAATAGTACTGCCACGGTGAATAATTCAGTTCT 1080
QY 1088 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTAATAACTTACTACTATGATGTCAC 1147
Db 1081 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTAATAACTTACTACTATGATGTCAC 1140
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Db 1141 ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAGAAAGAAACAAATCAGCTTCAGAGACTG 1200
QY 1208 TGCTGAAGTATTCAAACTCAGGACACACCAAAATGGCATCTACAGTTAAACATTCCTTAA 1267
Db 1201 TGCTGAAGTATTCAAACTCAGGACACACCAAAATGGCATCTACAGTTAAACATTCCTTAA 1260
QY 1268 TTCTACAGAAGAGATCAAGGCCCTACTGTGACATGGAAGCTGGAGGCGGGTGACAAAT 1327
Db 1261 TTCTACAGAAGAGATCAAGGCCCTACTGTGACATGGAAGCTGGAGGCGGGTGACAAAT 1320
QY 1328 TATTACGACGCTGAGGATGGACGGTGTGATTTTCAGAGGACTTGGAAAGATATAAAGT 1387
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QY 1388 GGGATTTGTTAACTTACAGGAGATATTGGCTGGGAATAGTTTGTTCGCAACTGAC 1447
Db 1381 GGGATTTGTTAACTTACAGGAGATATTGGCTGGGAATAGTTTGTTCGCAACTGAC 1440
QY 1448 TAATCAGCAACGCTATGTGCTTTAAATAACCTTAAAGACTGGGAAGGAATGAGGCTTA 1507
Db 1441 TAATCAGCAACGCTATGTGCTTTAAATAACCTTAAAGACTGGGAAGGAATGAGGCTTA 1500
QY 1508 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1567
Db 1501 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1560
QY 1568 AGGACTTACAGGACAGCCGCAAAATAGCAGCATCAGCCCAACGAGGAATGATTTTAG 1627
Db 1561 AGGACTTACAGGACAGCCGCAAAATAGCAGCATCAGCCCAACGAGGAATGATTTTAG 1620
QY 1628 CACAAAGGATGGAGACAAACGACAAATGTATTGCAAAATGTTTCAAAATGCTTAACAGGAGG 1687
Db 1621 CACAAAGGATGGAGACAAACGACAAATGTATTGCAAAATGTTTCAAAATGCTTAACAGGAGG 1680
QY 1688 CTGGTGGTTTGATGCATGTGGTCTTCCAACTTGGAACGGAATGTACTATCCACAGAGGCA 1747
Db 1681 CTGGTGGTTTGATGCATGTGGTCTTCCAACTTGGAACGGAATGTACTATCCACAGAGGCA 1740
QY 1748 GAAACAAATAAGTTCAACGGCAATTAATGGTACTACTGGAAGGCTCAGGCTATTTCGCT 1807
Db 1741 GAAACAAATAAGTTCAACGGCAATTAATGGTACTACTGGAAGGCTCAGGCTATTTCGCT 1800
QY 1808 CAAGGCCAACACCATGATATCCGACCAAGAGATTTCTTAAACATCCCACTGACCTGAGG 1867
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Db 1801 CAAGGCCAACACCATGATATCCGACCAAGAGATTTCTTAAACATCCCACTGATCCCACTGAGG 1860
QY 1868 AACTGTCTCGAACTATATTTTCAAAAGACTTAAAGCCAGTGCACCTGAAAGTCA CGGCTGGCA 1927
Db 1861 AACTGTCTCGAACTATATTTTCAAAAGACTTAAAGCCAGTGCACCTGAAAGTCA CGGCTGGCA 1920
QY 1928 CTGTGCTCTCTTCCACCAAGAGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1987
Db 1921 CTGTGCTCTCTTCCACCAAGAGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1980
QY 1988 GATTAGAGCCTGTAAACCTTATCATTAAACTTGAATCATTGATCATTAAACGGACCAAGCAAGAC 2047
Db 1981 GATTAGAGCCTGTAAACCTTATCATTAAACTTGAATCATTGATCATTAAACGGACCAAGCAAGAC 2040
QY 2048 CCTAAACATCCATATTCGTGATTAGACAGAACACCTATGCAAAAGATGAACCCGAGGCTGA 2107
Db 2041 CCTAAACATCCATATTCGTGATTAGACAGAACACCTATGCAAAAGATGAACCCGAGGCTGA 2100
QY 2108 GAATCAGACTGACAGTGTTCACAGACGCTGCTGTCAACAACCAAGAAATGTTATGTGCAAGTTT 2167
Db 2101 GAATCAGACTGACAGTGTTCACAGACGCTGCTGTCAACAACCAAGAAATGTTATGTGCAAGTTT 2160
QY 2168 ATCAGTAAATTAACCTGGAACCAAGAACATTTATGTTATATACATACAGATCATCTTGGAACT 2227
Db 2161 ATCAGTAAATTAACCTGGAACCAAGAACATTTATGTTATATCAATACAGATCATCTTGGAACT 2220
QY 2228 GCATTTCTCTGAGCACTGTTTATACACTGTGTAAATATCCCATATGTCCT 2276
Db 2221 GCATTTCTCTGAGCACTGTTTATACACTGTGTAAATATCCCATATGTCCT 2269
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RESULT 11
US-10-101-510-460
; Sequence 460, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117, 0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 460
; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-460
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Query Match 99.4%; Score 2269; DB 15; Length 2269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 8 TGGGTGGTGGTTTATCTCTCCAGCCTTGAGGAGGGAACAACACTGTAGGATCTGGGG 67
Db 1 TGGGTGGTGGTTTATCTCTCCAGCCTTGAGGAGGGAACAACACTGTAGGATCTGGGG 60
QY 68 AGAGAGGAACAAGGACCGTGAAAGCTGCTCTGTAAAAAGCTGACACAGCCCTCCCAAGTG 127
Db 61 AGAGAGGAACAAGGACCGTGAAAGCTGCTCTGTAAAAAGCTGACACAGCCCTCCCAAGTG 120
QY 128 AGCAGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGCTGAGGAGAACACAG 187
Db 121 AGCAGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGCTGAGGAGAACACAG 180
QY 188 CAGTAAAAACCAAGGTTTCTACTGGAAGGAGGAAAGAGAGAGACTTTTCATTGACGACC 247
Db 181 CAGTAAAAACCAAGGTTTCTACTGGAAGGAGGAAAGAGAGAGACTTTTCATTGACGACC 240
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|    |      |   |      |
|----|------|---|------|
| Qy | 248  | CAGCCATGGCAGCGGTAGCAGCCCTCGGTTTTCAGACGGCAGCAGCTCGGAGCTCTGGACGTT   | 307  |
| Db | 241  | CAGCCATGGCAGCGGTAGCAGCCCTCGGTTTTCAGACGGCAGCAGCTCGGAGCTCTGGACGTT   | 300  |
| Qy | 308  | GTGCTTTGGCCCTCAAGTTTTCGTAAGCTGCTGGTTTATTACTGAAGAAAGAAATGTGCGCAGAT | 367  |
| Db | 301  | GTGCTTTGGCCCTCAAGTTTTCGTAAGCTGCTGGTTTATTACTGAAGAAAGAAATGTGCGCAGAT | 360  |
| Qy | 368  | TGTTTTCTTTTACTCTCAGAGCTGTGATCTTGCTTTGGCCGAGGCTATAACAACTTTTCGGAA   | 427  |
| Db | 361  | TGTTTTCTTTTACTCTCAGAGCTGTGATCTTGCTTTGGCCGAGGCTATAACAACTTTTCGGAA   | 420  |
| Qy | 428  | GAGCATGGGACAGCATATAGGAAGAAGCAATATCAGGTCCAGCATGGGTCTCGCAGCTACAC    | 487  |
| Db | 421  | GAGCATGGGACAGCATATAGGAAGAAGCAATATCAGGTCCAGCATGGGTCTCGCAGCTACAC    | 480  |
| Qy | 488  | TTTTCTCTCTCCAGAGATGGACAACCTCGCGCTCTTCTCCAGCCCTCTAGCTGTCCAATGCG    | 547  |
| Db | 481  | TTTTCTCTCTCCAGAGATGGACAACCTCGCGCTCTTCTCCAGCCCTCTAGCTGTCCAATGCG    | 540  |
| Qy | 548  | TGTGCGAGGGGACGCGCGCTCGAATACGATGCTCGGTGCGAGGCTCGAAGTGTGGA          | 607  |
| Db | 541  | TGTGCGAGGGGACGCGCGCTCGAATACGATGCTCGGTGCGAGGCTCGAAGTGTGGA          | 600  |
| Qy | 608  | GAAATCATGTGGAAAAAACHACTCAGTGGCTTAATGAAGCTTGAGAAATTAATCCAGGACAA    | 667  |
| Db | 601  | GAAATCATGTGGAAAAAACHACTCAGTGGCTTAATGAAGCTTGAGAAATTAATCCAGGACAA    | 660  |
| Qy | 668  | CATGAAGAAGAATGTTAGAGATACAGCAGAAATGCAGTACAGAACCGACGCGCTGTGAT       | 727  |
| Db | 661  | CATGAAGAAGAATGTTAGAGATACAGCAGAAATGCAGTACAGAACCGACGCGCTGTGAT       | 720  |
| Qy | 728  | GATAGAATAAGGGACAAACCTGTTTGAACCAAAACAGCTGAGCAAAACCGGAAGTTAACTGA    | 787  |
| Db | 721  | GATAGAATAAGGGACAAACCTGTTTGAACCAAAACAGCTGAGCAAAACCGGAAGTTAACTGA    | 780  |
| Qy | 788  | TGTGGGAGCCCAAGTATTAATTCAGACCGAGACTTGAACTTCAGCTCTTGGAACACTC        | 847  |
| Db | 781  | TGTGGGAGCCCAAGTATTAATTCAGACCGAGACTTGAACTTCAGCTCTTGGAACACTC        | 840  |
| Qy | 848  | CCTCTCCAGCAAAACAAATTTGGAAAAACAGATTTTGGACCGACCCAGCTGAAATAAACAAAT   | 907  |
| Db | 841  | CCTCTCCAGCAAAACAAATTTGGAAAAACAGATTTTGGACCGACCCAGCTGAAATAAACAAAT   | 900  |
| Qy | 908  | GCAAGATAAGAACAGATTTCTTAGAAAAAGAGGTGCTAGCTATGGAAGACAGCACATCAT      | 967  |
| Db | 901  | GCAAGATAAGAACAGATTTCTTAGAAAAAGAGGTGCTAGCTATGGAAGACAGCACATCAT      | 960  |
| Qy | 968  | CCAACTACAGTCAATATAAAGAGAGAAGATTCAGCTACAGGTGTTAGTATCCCAAGCAAAA     | 1027 |
| Db | 961  | CCAACTACAGTCAATATAAAGAGAGAAGATTCAGCTACAGGTGTTAGTATCCCAAGCAAAA     | 1020 |
| Qy | 1028 | TTCCATCATTTGAAGAACTAGAAAAAAAATAGTGACTGCCACGGTGAATAAATTCAGTTCT     | 1087 |
| Db | 1021 | TTCCATCATTTGAAGAACTAGAAAAAAAATAGTGACTGCCACGGTGAATAAATTCAGTTCT     | 1080 |
| Qy | 1088 | TCAAAAGCAGCAACATGATCTCATCGGAGACAGTTTAATAACTTACTGACTATGATGTCAC     | 1147 |
| Db | 1081 | TCAAAAGCAGCAACATGATCTCATCGGAGACAGTTTAATAACTTACTGACTATGATGTCAC     | 1140 |
| Qy | 1148 | ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAGAAACAAATCAGCTTCAGAGACTG     | 1207 |
| Db | 1141 | ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAGAAACAAATCAGCTTCAGAGACTG     | 1200 |
| Qy | 1208 | TGCTGNAAGTATTCAAATCAGGACACACCAAAATGGCATCTACACGTTTAACTTCCCTAA      | 1267 |
| Db | 1201 | TGCTGNAAGTATTCAAATCAGGACACACCAAAATGGCATCTACACGTTTAACTTCCCTAA      | 1260 |
| Qy | 1268 | TTCTACAGAAGAGATCAAGGCTACTGTGACATGGAAAGCTGGAGGAGCGGGTGGACAAT       | 1327 |
| Db | 1261 | TTCTACAGAAGAGATCAAGGCTACTGTGACATGGAAAGCTGGAGGAGCGGGTGGACAAT       | 1320 |
| Qy | 1328 | TATTCAGCGCAGTGGAGATGCGCGTTGATTTTTCAGAGGACTTTGGAAAAAGATATAAAGT     | 1387 |

RESULT 12

RESOL 12  
US-10-373-561-3US-10-373-361-3  
: Sequence 3. Application us/10373561

US20030175276A1

; PUBLICATION NO: US20  
; GENERAL INFORMATION:  
; GENERAL INFORMATION:

ADDITIONAL INFORMATION:

APPLICANT: Phillip E. Thorpe

APPLICANT: ROLF A. BREKKEN

; TITLE OF INVENTION: ANTIBOD



; CURRENT APPLICATION NUMBER: US/10/373,561
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/561,499
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/131,432
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-373-561-3

Query Match 99.4%; Score 2269; DB 16; Length 2269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGGTTGGTGTATCTCTCCAGCCTTTGAGGGAGGGAACAACACTGTAGGATCTGGGG 67
DB 1 TGGGTTGGTGTATCTCTCCAGCCTTTGAGGGAGGGAACAACACTGTAGGATCTGGGG 60

QY 68 AGAGAGGAACAAGGACCTGAAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG 127
DB 61 AGAGAGGAACAAGGACCTGAAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG 120

QY 128 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTCTTACTGCAATGCTGCGATGCTGAGAGAAACACAG 187
DB 121 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTCTTACTGCAATGCTGCGATGCTGAGAGAAACACAG 180

QY 188 CAGTAAAAACAGGTTGTCTACGGAAGGAGGAAAGAGACTTTTCATTGACGGACC 247
DB 181 CAGTAAAAACAGGTTGTCTACGGAAGGAGGAAAGAGAGACTTTTCATTGACGGACC 240

QY 248 CAGCCATGCGAGGTAGCAGCCCTGCTGTTTCAGACGGCAGAGCTCGGACCTCTGGAAGT 307
DB 241 CAGCCATGCGAGGTAGCAGCCCTGCTGTTTCAGACGGCAGAGCTCGGACCTCTGGAAGT 300

QY 308 GTGTTTGCCCTCAAGTTTCTAAGCTGCTGGTTTATTACTGAAAGAAAGTGTGGCAGAT 367
DB 301 GTGTTTGCCCTCAAGTTTCTAAGCTGCTGGTTTATTACTGAAAGAAAGTGTGGCAGAT 360

QY 368 TGTGTTCTTTA CTGAGCTGTGATCTTCTGTCGCGCCAGCCTATAACAACTTTTCGGAA 427
DB 361 TGTGTTCTTTA CTGAGCTGTGATCTTCTGTCGCGCCAGCCTATAACAACTTTTCGGAA 420

QY 428 GAGCATGGACACATAGGAAGAAGCAATATCAGGTCAGCATGGGTCCTGCGACTACAC 487
DB 421 GAGCATGGACACATAGGAAGAAGCAATATCAGGTCAGCATGGGTCCTGCGACTACAC 480

QY 488 TTTTCTCTGCGCAGAGATGGAACAACCTGCGCTCTTCTCAGCCCTCAGTGTGCAATGC 547
DB 481 TTTTCTCTGCGCAGAGATGGAACAACCTGCGCTCTTCTCAGCCCTCAGTGTGCAATGC 540

QY 548 TGTGACAGGGACGCGCCGCTCGAATACGATGACTCGGTGCGAGAGCTGCAAGTGTGGA 607
DB 541 TGTGACAGGGACGCGCCGCTCGAATACGATGACTCGGTGCGAGAGCTGCAAGTGTGGA 600

QY 608 GAACATCATGGAAGAAACAACACTCAGTGGCTAATGAGCTTGAGATTATATCCAGCAAA 667
DB 601 GAACATCATGGAAGAAACAACACTCAGTGGCTAATGAGCTTGAGATTATATCCAGCAAA 660

QY 668 CATGAAGAAAGAAATGGTAGAGATACAGCAGAAATGCAATGAGTACAGAACCCAGCGCTGTGAT 727
DB 661 CATGAAGAAAGAAATGGTAGAGATACAGCAGAAATGCAATGAGTACAGAACCCAGCGCTGTGAT 720

QY 728 GATAGAAATAGGGAACAACTGTTGAA CCAAA CAGCTGAGGAAACCGCGAAATTAACATGA 787
DB 721 GATAGAAATAGGGAACAA CTTGTTGAA CCAAA CAGCTGAGGAAACCGCGAAATTAACATGA 780

QY 788 TGTGGAAGCCCAAGTATTAAATCAGACACAGAGACTTGAATCTTACGCTCTTGGAAACATTC 847
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QY 848 CCTCTCGACAAACAAATTGGAAAAACAGATTTTGGACGAGCCAGTGAAATATAACAAAT 907
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QY 908 GCAAGATAAGAACAGTTTCTCTAGAAAAAGAGGTGTAGCTATGGAAGACAAACACATCAT 967
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QY 968 CCAACTACAGTCAATATAAGAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAACAAA 1027
DB 961 CCAACTACAGTCAATATAAGAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAACAAA 1020

QY 1028 TTTCCATCATTTGAAGAACTAGAAAAAAAATAGTGTGCTGACCGGTGAAATAATTCAGTTCT 1087
DB 1021 TTTCCATCATTTGAAGAACTAGAAAAAAAATAGTGTGCTGACCGGTGAAATAATTCAGTTCT 1080

QY 1088 TCANAAGCAGCAACATGATCTCATGGAGACAGTTTAATACTTAATCTGACTATGATGTCCAC 1147
DB 1081 TCANAAGCAGCAACATGATCTCATGGAGACAGTTTAATACTTAATCTGACTATGATGTCCAC 1140

QY 1148 ATCAAACTCAGCTAAGGACCCCACTGTTGCTAAAGAAACAAATCAGCTTCAGAGACTG 1207
DB 1141 ATCAAACTCAGCTAAGGACCCCACTGTTGCTAAAGAAACAAATCAGCTTCAGAGACTG 1200

QY 1208 TGCTGAAGTATTTCAAATCAGGACACACCAAAATGGCATCTACAGTTTAAACATTCCTTAA 1267
DB 1201 TGCTGAAGTATTTCAAATCAGGACACACCAAAATGGCATCTACAGTTTAAACATTCCTTAA 1260

QY 1268 TTCTACAGAAGAGATCAAGGCCCTACTGTGACATGGAAGCTGGAGAGCGGGTGACAAAT 1327
DB 1261 TTCTACAGAAGAGATCAAGGCCCTACTGTGACATGGAAGCTGGAGAGCGGGTGACAAAT 1320

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QY 1388 GGGATTGCTGAACCTCTCAGGAGAAATATGGCTGGGAAATGAGTTTGTTCGCAACTGCAC 1447
DB 1381 GGGATTGCTGAACCTCTCAGGAGAAATATGGCTGGGAAATGAGTTTGTTCGCAACTGCAC 1440

QY 1448 TAATCAGCAACCGCTATGCTTTAAATACACCTTAAAGCTGGGAAGGAATGAGGCTTA 1507
DB 1441 TAATCAGCAACCGCTATGCTTTAAATACACCTTAAAGCTGGGAAGGAATGAGGCTTA 1500

QY 1508 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATAGGATTCACCTTAA 1567
DB 1501 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATAGGATTCACCTTAA 1560

QY 1568 AGGACTTACAGGACAGCGGCAAAATTAAGCAGCATCAGCCAAACCCAGGAAATGATTTTAG 1627
DB 1561 AGGACTTACAGGACAGCGGCAAAATTAAGCAGCATCAGCCAAACCCAGGAAATGATTTTAG 1620

QY 1628 CACAAAGGATGAGGACAAACGAAATGTATTGCAAAATGTTTCAAAAATGCTTAACAGGAGG 1687
DB 1621 CACAAAGGATGAGGACAAACGAAATGTATTGCAAAATGTTTCAAAAATGCTTAACAGGAGG 1680

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DB 1681 CTGGTGGTTGATGATGCTGTTCTTCCAACTTGAACCGAAATGTACTATCCACAGAGGCA 1740

QY 1748 GAACACAAATTAAGTTCAACCGCATTTAAATGGTACTATCTGGAAGGCTCAGGCTATTCGCT 1807
DB 1741 GAACACAAATTAAGTTCAACCGCATTTAAATGGTACTATCTGGAAGGCTCAGGCTATTCGCT 1800

QY 1808 CAAAGCCCAACCAATGATGATCCGACGAGAGATTTCTAAACATCCAGTCCACCTGAGG 1867
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QY 1868 AACTGCTCGAATATTTTCAAGAGCTTTAAGCCAGTGCACCTGAAAGTCAACGGCTGCGCA 1927
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QY 1928 CTGTGCTCTTCCACACAGAGGGCGTGTGCTCGGTGCTGACGGACCCACATGCTCCA 1987  
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DB 1981 GATTAGAGCGCTGTAACCTTTATCACTTAACTTGAATCACTTAAACGGACCAAGCAAGAC 2040  
QY 2048 CCTAAACATCCATAATTTGTAATAGACAGAACACCTATGCAAAAGATGAACCCGAGCTGA 2107  
DB 2041 CCTAAACATCCATAATTTGTAATAGACAGAACACCTATGCAAAAGATGAACCCGAGCTGA 2100  
QY 2108 GAATCAGACTGACAGTTTACAGACGCTGCTGTGTACAAACCAAGATGTTATGTCAGATTT 2167  
DB 2101 GAATCAGACTGACAGTTTACAGACGCTGCTGTGTACAAACCAAGATGTTATGTCAGATTT 2160  
QY 2168 ATCAGTAATAACTCGGAACACAGACACTTATGTTATACAAATACAGATCATCTTGGAACT 2227  
DB 2161 ATCAGTAATAACTCGGAACACAGACACTTATGTTATACAAATACAGATCATCTTGGAACT 2220  
QY 2228 GCATTCTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCCT 2276  
DB 2221 GCATTCTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCCT 2269

RESULT 13  
US-10-317-803-18  
; Sequence 18, Application US/10317803  
; Publication No. US20040115640A1  
; GENERAL INFORMATION:  
; APPLICANT: Kathleen Myers  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: MODULATION OF ANGIOPOIETIN-2 EXPRESSION  
; FILE REFERENCE: RTS-0454  
; CURRENT APPLICATION NUMBER: US/10/317,803  
; CURRENT FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 244  
; SEQ ID NO 18  
; LENGTH: 2269  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (350)...(1840)  
US-10-317-803-18

Query Match 99.4%; Score 2269; DB 19; Length 2269;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGTTTGGTGTATCTCTCCAGCCTTGAGGAGGGGAACAACACTGTAGGATCTGGGG 67  
DB 1 TGGTTTGGTGTATCTCTCCAGCCTTGAGGAGGGGAACAACACTGTAGGATCTGGGG 60  
QY 68 AGAGAGGAACAAGAGCCGCTGAAAGCTGCTGTGTAAGCTGACACAGCCCTCCCAAGTG 127  
DB 61 AGAGAGGAACAAGAGCCGCTGAAAGCTGCTGTGTAAGCTGACACAGCCCTCCCAAGTG 120  
QY 128 AGCAGGACTGTTCTCCAGCTGCAATCTGACAGTTTACTGCATGCTGGAGAGACACAG 187  
DB 121 AGCAGGACTGTTCTCCAGCTGCAATCTGACAGTTTACTGCATGCTGGAGAGACACAG 180  
QY 188 CAGTAAAAACAGGTTTGTCTACTCGAAAAAGAGAAAGAGAACTTTCATTGACGGACC 247  
DB 181 CAGTAAAAACAGGTTTGTCTACTGGAANAAGAGAGAGAGAACTTTCATTGACGGACC 240  
QY 248 CAGCCATGGCAGCGTAGCAGCCCTGCGTTTCAGACGCGCAGCTCGGAGCTCTGGACGT 307  
DB 241 CAGCCATGGCAGCGTAGCAGCCCTGCGTTTCAGACGCGCAGCTCGGAGCTCTGGACGT 300  
QY 308 GTGTTTGGCCCTCAAGTTTGTCTAAGCTGCTGTTTATTACTGAAGAAAGATGTGGCAGAT 367  
DB 301 GTGTTTGGCCCTCAAGTTTGTCTAAGCTGCTGTTTATTACTGAAGAAAGATGTGGCAGAT 360

QY 368 TGTTCCTTTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCCTATAACAACCTTTTCGGA 427  
DB 361 TGTTCCTTTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCCTATAACAACCTTTTCGGA 420  
QY 428 GAGCATGGACAGCATAGGAAGAAGCAATATCAGGTCCAGCATGGGTCTCTGCAAGCTACAC 487  
DB 421 GAGCATGGACAGCATAGGAAGAAGCAATATCAGGTCCAGCATGGGTCTCTGCAAGCTACAC 480  
QY 488 TTTCTCTCTGCCAGAGATGGACAACTGCGGCTCTTCTCAGGCCCTACGTGTCCAATGC 547  
DB 481 TTTCTCTCTGCCAGAGATGGACAACTGCGGCTCTTCTCAGGCCCTACGTGTCCAATGC 540  
QY 548 TGTGACAGAGGAGCGCCGCTCGAATACGATGACTCGGTGCAGAGCTGCAAGTGTCTGA 607  
DB 541 TGTGACAGAGGAGCGCCGCTCGAATACGATGACTCGGTGCAGAGCTGCAAGTGTCTGA 600  
QY 608 GAACATCATGGAAGAAACAACACTCAGTGGCTTAATGAAGCTTGAGAAATATATCCAGGACAA 667  
DB 601 GAACATCATGGAAGAAACAACACTCAGTGGCTTAATGAAGCTTGAGAAATATATCCAGGACAA 660  
QY 668 CATGAAGAAGAAATGTTAGAGATACAGCAGAAATGCAGTACAGAACCCAGCGCTGTGAT 727  
DB 661 CATGAAGAAGAAATGTTAGAGATACAGCAGAAATGCAGTACAGAACCCAGCGCTGTGAT 720  
QY 728 GATAGAAATAGGGACAAACCTGTTGAACCAACAGCTGAGCAACCGGGAAGTTAACTGA 787  
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QY 788 TGTGGAAGCCCAAGTATTAAATCAGACCCAGCAGACTTGAACCTTCAGCTCTTGGAACTC 847  
DB 781 TGTGGAAGCCCAAGTATTAAATCAGACCCAGCAGACTTGAACCTTCAGCTCTTGGAACTC 840  
QY 848 CCTCTCGACAAACAAATTTGGAAGAAACAGATTTTGGACCCAGCAGTGAATAACAAAT 907  
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QY 908 GCAAGATAGAACAGTTTCTAGAAAAGAGGTGCTAGCTATGGAAGACAGCAGCATCAT 967  
DB 901 GCAAGATAGAACAGTTTCTAGAAAAGAGGTGCTAGCTATGGAAGACAGCAGCATCAT 960  
QY 968 CCAACTACAGTCAATATAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAAGCAAAA 1027  
DB 961 CCAACTACAGTCAATATAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAAGCAAAA 1020  
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DB 1021 TTCCATCATTTGAAGAACTAGAAAAAATAGTGACTGCCACGCTGAATAATTCAGTTCT 1080  
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DB 1141 ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAGAGAAATCAGCTTCAGAGACTG 1200  
QY 1208 TGCTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTACACGTTAAACATTCCTTAA 1267  
DB 1201 TGCTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTACACGTTAAACATTCCTTAA 1260  
QY 1268 TTCTACAGAAAGAGATCAAGGCCTACTGTGACATGGAAGCTGGAGGAGCGGGTGGACAT 1327  
DB 1261 TTCTACAGAAAGAGATCAAGGCCTACTGTGACATGGAAGCTGGAGGAGCGGGTGGACAT 1320  
QY 1328 TATTTCAGGACGCTGAGGATGCGAGCTGTTGATTTTCAGAGGACTTGGAAAGAAATAAAGT 1387  
DB 1321 TATTTCAGGACGCTGAGGATGCGAGCTGTTGATTTTCAGAGGACTTGGAAAGAAATAAAGT 1380  
QY 1388 GGGATTTGGTAAACCTTTTCAGGAGAAATATGGCTGGGAAATGAGTTTGTTCGCAACTGAC 1447  
DB 1381 GGGATTTGGTAAACCTTTTCAGGAGAAATATGGCTGGGAAATGAGTTTGTTCGCAACTGAC 1440

1448 TAATCAGCAACGCTATGTGCTTAAATAACACCTTAAAGACTGGGAAGGAAATGAGGCTTA 1507  
Db TAATCAGCAACGCTATGTGCTTAAATAACACCTTAAAGACTGGGAAGGAAATGAGGCTTA 1500  
QY 1508 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTATAGATTCACTTAA 1567  
Db CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTATAGATTCACTTAA 1560  
QY 1568 AGGACTTACAGGGACACGCGGCAAAATAAGCAGCATCAGCAACACAGGAAATGATTTAG 1627  
Db AGGACTTACAGGGACACGCGGCAAAATAAGCAGCATCAGCAACACAGGAAATGATTTAG 1620  
QY 1628 CACAAAGGATGAGACAAACGAAATGTATTTGCAAAATGTTTCAAAATGCTTACAGGAG 1687  
Db CACAAAGGATGAGACAAACGAAATGTATTTGCAAAATGTTTCAAAATGCTTACAGGAG 1680  
QY 1688 CTGGTGTTTGTATGATGTGCTTCCAACTTGAACGGAATGTACTATCCACAGAGCA 1747  
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QY 1808 CAAAGGCCAACCATGATGATCGGACGAGAGATTTCTAAACATCCAGTCCACCTGAGG 1867  
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QY 1868 AACTGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCACTGAAAGTCAACGGCTGCGCA 1927  
Db AACTGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCACTGAAAGTCAACGGCTGCGCA 1920  
QY 1928 CTGTGTCTCTTCCACACAGAGGGGCTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1987  
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QY 1988 GATTAGAGCTGTAAACTTTATCACTTAACTTGAATGATCTTAAACGGAACCAAGCAAGAC 2047  
Db GATTAGAGCTGTAAACTTTATCACTTAACTTGAATGATCTTAAACGGAACCAAGCAAGAC 2040  
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QY 2108 GAATCAGACTGACAGTTTACAGACGCTGCTGTACAAACCAAGAAATGTTATGTCGAAGTTT 2167  
Db GAATCAGACTGACAGTTTACAGACGCTGCTGTACAAACCAAGAAATGTTATGTCGAAGTTT 2160  
QY 2168 ATCAGTAAATTAAGTGAACAGACACTTATGTTATACAAATACAGATCATCTTGGAACT 2227  
Db ATCAGTAAATTAAGTGAACAGACACTTATGTTATACAAATACAGATCATCTTGGAACT 2220  
QY 2228 GCATTTCTTGAGCACTGTTTATACACTGTGTAATATACCATATGTCCT 2276  
Db GCATTTCTTGAGCACTGTTTATACACTGTGTAATATACCATATGTCCT 2269

RESULT 14  
US-10-789-222-33  
; Sequence 33, Application US/10789222  
; Publication No. US20040186054A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Qin  
; TITLE OF INVENTION: of the Same  
; FILE REFERENCE: UPN0003-100 (P3115)  
; CURRENT APPLICATION NUMBER: US/10789,222  
; PRIOR FILING DATE: 2004-02-27  
; PRIOR APPLICATION NUMBER: US 60/450,582  
; PRIOR FILING DATE: 2003-02-27  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 33

; LENGTH: 2269  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-789-222-33

Query Match 99.4%; Score 2269; DB 19; Length 2269;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGGTTGGTGGTTTATCTCTCTCCAGCCTTGGAGGAGGAAACAACACTGTAGGATCTGGGG 67  
Db TGGGTTGGTGGTTTATCTCTCTCCAGCCTTGGAGGAGGAAACAACACTGTAGGATCTGGGG 60  
QY 68 AGAGAGGAACAAGACCGTGAAGCTGCTCTGTAAAAAGCTGACACAGCCCTCCCAAGTG 127  
Db AGAGAGGAACAAGACCGTGAAGCTGCTCTGTAAAAAGCTGACACAGCCCTCCCAAGTG 120  
QY 128 AGCAGACTGTCTTCCACTGCAATCTGACAGTTTACTGATGCTGGAGAGAACAG 187  
Db AGCAGACTGTCTTCCACTGCAATCTGACAGTTTACTGATGCTGGAGAGAACAG 180  
QY 188 CAGTAAAAACCAAGGTTTGTCTACTGAAAAAGAGAAAGAGAGACTTTTCATTGACGGACC 247  
Db CAGTAAAAACCAAGGTTTGTCTACTGAAAAAGAGAAAGAGAGACTTTTCATTGACGGACC 240  
QY 248 CAGCCATGCGCAGCTGAGCAGCCCTGCGTTTCAGACGGCAGCAGCTCGGACCTCTGACGCT 307  
Db CAGCCATGCGCAGCTGAGCAGCCCTGCGTTTCAGACGGCAGCAGCTCGGACCTCTGACGCT 300  
QY 308 GTGTTTGGCCTCAAGTTTGTCTAAGCTGTGTTTATTAAGTGAAGAAAGATGTGTCAGAT 367  
Db GTGTTTGGCCTCAAGTTTGTCTAAGCTGTGTTTATTAAGTGAAGAAAGATGTGTCAGAT 360  
QY 368 TGTGTTTCTTACTCTGAGCTGTGATCTTGTCTGTCGCGCAGCTTAAACAACCTTTGCGAA 427  
Db TGTGTTTCTTACTCTGAGCTGTGATCTTGTCTGTCGCGCAGCTTAAACAACCTTTGCGAA 420  
QY 428 GAGCATGGAACGATAGGAAAGAAAGCAATATCAGGTCAGCATGCGTCTCGAGCTACAC 487  
Db GAGCATGGAACGATAGGAAAGAAAGCAATATCAGGTCAGCATGCGTCTCGAGCTACAC 480  
QY 488 TTTCTCTCTGCGCAGAGTGGACAACTGCGCTCTCTCTCCAGCCCTCAGTGTCCAATGC 547  
Db TTTCTCTCTGCGCAGAGTGGACAACTGCGCTCTCTCTCCAGCCCTCAGTGTCCAATGC 540  
QY 548 TGTGCAAGGGAACGCGCGCTCGAATACGATGACTCGGTGCGAGGCTGCAAGTCTCGA 607  
Db TGTGCAAGGGAACGCGCGCTCGAATACGATGACTCGGTGCGAGGCTGCAAGTCTCGA 600  
QY 608 GAACATCATGGAACAAACACTCTCAGTGGCTTAATGAAGCTTGAAGATTAATATCCAGCA 667  
Db GAACATCATGGAACAAACACTCTCAGTGGCTTAATGAAGCTTGAAGATTAATATCCAGCA 660  
QY 668 CATGGAAGAAAGAAATGTTAGAGATACAGCAGAAATGCAATGACAGACGAGGCTGTGAT 727  
Db CATGGAAGAAAGAAATGTTAGAGATACAGCAGAAATGCAATGACAGACGAGGCTGTGAT 720  
QY 728 GATAGAAATAGGGCAAAACCTGTTGAAACCAACAGCTGAGCAAAACGCGAAGTTAACTGA 787  
Db GATAGAAATAGGGCAAAACCTGTTGAAACCAACAGCTGAGCAAAACGCGAAGTTAACTGA 780  
QY 788 TGTGGAAGCCCAAGTATTAAATCAGACCAAGAGCTTGAACTTTCAGCTCTTGGAAACATC 847  
Db TGTGGAAGCCCAAGTATTAAATCAGACCAAGAGCTTGAACTTTCAGCTCTTGGAAACATC 840  
QY 848 CCTCTCGACAAACAAATTTGGAAACAGATTTTGGACCAGACCCAGTGAATAAACAAT 907  
Db CCTCTCGACAAACAAATTTGGAAACAGATTTTGGACCAGACCCAGTGAATAAACAAT 900  
QY 908 GCAAGATAAGAACAGTTTCTTAGAAAAAGAGGTGTAGCTATGGAAGACAGACATCAT 967  
Db GCAAGATAAGAACAGTTTCTTAGAAAAAGAGGTGTAGCTATGGAAGACAGACATCAT 960



|    |      |  |      |
|----|------|--|------|
| QY | 428  | GAGCATGGACAGCATAGGAAGAAGCAATATCAGGTCCAGCATGGGTCTCGAGCTTACAC    | 487  |
| Db |      |  |      |
| QY | 421  | GAGCATGGACAGCATAGGAAGAAGCAATATCAGGTCCAGCATGGGTCTCGAGCTTACAC    | 480  |
| Db |      |  |      |
| QY | 488  | TTTCTCTCTCCGACAGATGGACAACTGCGCTCTTCTCCAGCCCTTACGTGTCCAAATGC    | 547  |
| Db |      |  |      |
| QY | 481  | TTTCTCTCTCCGACAGATGGACAACTGCGCTCTTCTCCAGCCCTTACGTGTCCAAATGC    | 540  |
| Db |      |  |      |
| QY | 548  | TGTGCAGAGGGAGCGCGCTCGAATACGATGACTCGGTGCAGAGGCTCGAAGTGTCTGA     | 607  |
| Db |      |  |      |
| QY | 541  | TGTGCAGAGGGAGCGCGCTCGAATACGATGACTCGGTGCAGAGGCTCGAAGTGTCTGA     | 600  |
| Db |      |  |      |
| QY | 608  | GAACTATCATCGAAAAACAACACTCAGTGGCTTAATGAAGCTTGAATAATATCCAGGACAA  | 667  |
| Db |      |  |      |
| QY | 601  | GAACTATCATGAAAAACAACACTCAGTGGCTTAATGAAGCTTGAATAATATCCAGGACAA   | 660  |
| Db |      |  |      |
| QY | 668  | CATGAAGAAAGAAATGGTATGAGATACAGACAGATGACATGACACAGACCGCTGTGTAT    | 727  |
| Db |      |  |      |
| QY | 661  | CATGAAGAAAGAAATGGTATGAGATACAGACAGATGACATGACACAGACCGCTGTGTAT    | 720  |
| Db |      |  |      |
| QY | 728  | GATAGAAATAGGGACAAAACCTGTTGAACCAACACAGCTGAGCAAAACGCGAAGTTAACTGA | 787  |
| Db |      |  |      |
| QY | 721  | GATAGAAATAGGGACAAAACCTGTTGAACCAACACAGCTGAGCAAAACGCGAAGTTAACTGA | 780  |
| Db |      |  |      |
| QY | 788  | TGTGGAAGCCCAAGTATTAAATCAGACACGAGACTTGAACCTTTCAGCTCTTGGAAACACTC | 847  |
| Db |      |  |      |
| QY | 781  | TGTGGAAGCCCAAGTATTAAATCAGACACGAGACTTGAACCTTTCAGCTCTTGGAAACACTC | 840  |
| Db |      |  |      |
| QY | 848  | CCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCAAGACAGTGAATAAACAATTT   | 907  |
| Db |      |  |      |
| QY | 841  | CCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCAAGACAGTGAATAAACAATTT   | 900  |
| Db |      |  |      |
| QY | 908  | GCAAGATAGAACAGTTTCTAGAAAGAGGTGCTAGCTATGGAAGACCAAGCAATCAT       | 967  |
| Db |      |  |      |
| QY | 901  | GCAAGATAGAACAGTTTCTAGAAAGAGGTGCTAGCTATGGAAGACCAAGCAATCAT       | 960  |
| Db |      |  |      |
| QY | 968  | CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTTACAGGTGTTAGTATCCAAGCAAAA    | 1027 |
| Db |      |  |      |
| QY | 961  | CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTTACAGGTGTTAGTATCCAAGCAAAA    | 1020 |
| Db |      |  |      |
| QY | 1028 | TTCCATCATGAGAACTAGAAAAAAAATAGTACTGCCACGGTGAATAATTCAGTTCT       | 1087 |
| Db |      |  |      |
| QY | 1021 | TTCCATCATGAGAACTAGAAAAAAAATAGTACTGCCACGGTGAATAATTCAGTTCT       | 1080 |
| Db |      |  |      |
| QY | 1088 | TCAAAGCAGCAACATGATCTCATGGAGACAGTTAATAACTTACTGACTATGATGTCCAC    | 1147 |
| Db |      |  |      |
| QY | 1081 | TCAAAGCAGCAACATGATCTCATGGAGACAGTTAATAACTTACTGACTATGATGTCCAC    | 1140 |
| Db |      |  |      |
| QY | 1148 | ATCAAACCTCAGCTAAGGACCCCACTGTTGCTAAAGAAAGCAAAATCAGCTTCCAGAGACTG | 1207 |
| Db |      |  |      |
| QY | 1141 | ATCAAACCTCAGCTAAGGACCCCACTGTTGCTAAAGAAAGCAAAATCAGCTTCCAGAGACTG | 1200 |
| Db |      |  |      |
| QY | 1208 | TGCTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTACAGTTAACTTCCCTTAA     | 1267 |
| Db |      |  |      |
| QY | 1201 | TGCTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTACAGTTAACTTCCCTTAA     | 1260 |
| Db |      |  |      |
| QY | 1268 | TTCTTACAGAAAGAGATCAAGCGCTTACTGTGACATGGAAGCTGGAGGAGGGGTGGACAA   | 1327 |
| Db |      |  |      |
| QY | 1261 | TTCTTACAGAAAGAGATCAAGCGCTTACTGTGACATGGAAGCTGGAGGAGGGGTGGACAA   | 1320 |
| Db |      |  |      |
| QY | 1328 | TATTTCAGCGACGTGAGGATGGCAGCGTGTGATTTTCAGAGGACTTGGAAAGAAATAAAGT  | 1387 |
| Db |      |  |      |
| QY | 1321 | TATTTCAGCGACGTGAGGATGGCAGCGTGTGATTTTCAGAGGACTTGGAAAGAAATAAAGT  | 1380 |
| Db |      |  |      |
| QY | 1388 | GGGATTTGGTAAACCTTCAGGAGAAATATGGCTGGGAATGATTTGTTCCGAACCTGAC     | 1447 |
| Db |      |  |      |
| QY | 1381 | GGGATTTGGTAAACCTTCAGGAGAAATATGGCTGGGAATGATTTGTTCCGAACCTGAC     | 1440 |
| Db |      |  |      |
| QY | 1448 | TAAATCAGCAACCGCTATGTCTTAAATAACACCTTAAAGACTGGGAAGGAAATGAGGCTTA  | 1507 |
| Db |      |  |      |
| QY | 1441 | TAAATCAGCAACCGCTATGTCTTAAATAACACCTTAAAGACTGGGAAGGAAATGAGGCTTA  | 1500 |
| Db |      |  |      |

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|----|------|---|------|
| QY | 1508 | CTCATTTGATGAACATTTTCTATCTCTCAAGTGAAGAACTCAATTTAGGATTCACCTTAA    | 1567 |
| Db |      |   |      |
| QY | 1501 | CTCATTTGATGAACATTTTCTATCTCTCAAGTGAAGAACTCAATTTAGGATTCACCTTAA    | 1560 |
| Db |      |   |      |
| QY | 1568 | AGGACTTACAGGGACAGCGCGCAAAATTAAGCAGCATCAGCCAAACCAAGGAAATGATTTAG  | 1627 |
| Db |      |   |      |
| QY | 1561 | AGGACTTACAGGGACAGCGCGCAAAATTAAGCAGCATCAGCCAAACCAAGGAAATGATTTAG  | 1620 |
| Db |      |   |      |
| QY | 1628 | CACAAAGGATGAGACAAACGACAAATGTATTTGCAAAATGTTTCAAAATGCTTAAACAGGAG  | 1687 |
| Db |      |   |      |
| QY | 1621 | CACAAAGGATGAGACAAACGACAAATGTATTTGCAAAATGTTTCAAAATGCTTAAACAGGAG  | 1680 |
| Db |      |   |      |
| QY | 1688 | CTGGTGGTTTGATGATGTGGTCTTCCAACTTGAACCGAAATGTACTATCCACAGAGGCA     | 1747 |
| Db |      |   |      |
| QY | 1681 | CTGGTGGTTTGATGATGTGGTCTTCCAACTTGAACCGAAATGTACTATCCACAGAGGCA     | 1740 |
| Db |      |   |      |
| QY | 1748 | GAAACAAATAAGTTCAACGGCATTTAAATGGTACTTACTGGAAAAGGCTCAGGCTATTCGCT  | 1807 |
| Db |      |   |      |
| QY | 1741 | GAAACAAATAAGTTCAACGGCATTTAAATGGTACTTACTGGAAAAGGCTCAGGCTATTCGCT  | 1800 |
| Db |      |   |      |
| QY | 1808 | CAAGGCCAACCAATGATGATCCGACACAGCAGATTTCTAAAACATCCAGTCCAACCTGAGG   | 1867 |
| Db |      |   |      |
| QY | 1801 | CAAGGCCAACCAATGATGATCCGACACAGCAGATTTCTAAAACATCCAGTCCAACCTGAGG   | 1860 |
| Db |      |   |      |
| QY | 1868 | AACTGTCTCGAACTATTTTCAAAGA CTTAAGCCCAAGTGCACTGAAAAGTCAACCGCTGCCA | 1927 |
| Db |      |   |      |
| QY | 1861 | AACTGTCTCGAACTATTTTCAAAGA CTTAAGCCCAAGTGCACTGAAAAGTCAACCGCTGCCA | 1920 |
| Db |      |   |      |
| QY | 1928 | CTGTGTCTCTTCCACCAACAGAGGGGGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA    | 1987 |
| Db |      |   |      |
| QY | 1921 | CTGTGTCTCTTCCACCAACAGAGGGGGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA    | 1980 |
| Db |      |   |      |
| QY | 1988 | GATTAGAGCCTGTAACCTTTTATCACTTAAACCTTGATCACTTAAACCTTAAACCTTAAAC   | 2047 |
| Db |      |   |      |
| QY | 1981 | GATTAGAGCCTGTAACCTTTTATCACTTAAACCTTGATCACTTAAACCTTAAACCTTAAAC   | 2040 |
| Db |      |   |      |
| QY | 2048 | CCTAAACATCCATAATTTGATTAGACAGAACACCTTATGCAAAAGATGAACCCGAGGCTGA   | 2107 |
| Db |      |   |      |
| QY | 2041 | CCTAAACATCCATAATTTGATTAGACAGAACACCTTATGCAAAAGATGAACCCGAGGCTGA   | 2100 |
| Db |      |   |      |
| QY | 2108 | GAAATCAGAGTACAGCTTTTACAGACGCTGCTGTCACAACCAAGAAATGTTATGTGCAAGTTT | 2167 |
| Db |      |   |      |
| QY | 2101 | GAAATCAGAGTACAGCTTTTACAGACGCTGCTGTCACAACCAAGAAATGTTATGTGCAAGTTT | 2160 |
| Db |      |   |      |
| QY | 2168 | ATCAGTAAATAACTGGAACCAAGAACACTTATGTTTATACAATACAGATCATCTTGGAACT   | 2227 |
| Db |      |   |      |
| QY | 2161 | ATCAGTAAATAACTGGAACCAAGAACACTTATGTTTATACAATACAGATCATCTTGGAACT   | 2220 |
| Db |      |   |      |
| QY | 2228 | GCATTTCTTCTGAGCACTGTTTATACACTGTGTGTAATAATACCCATATGTCCT          | 2276 |
| Db |      |   |      |
| QY | 2221 | GCATTTCTTCTGAGCACTGTTTATACACTGTGTGTAATAATACCCATATGTCCT          | 2269 |
| Db |      |   |      |

Search completed: July 29, 2005, 10:42:15  
Job time : 2046.78 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 02:36:24 ; Search time 2288.57 Seconds  
(without alignments)  
10777.765 Million cell updates/sec

Title: US-10-603-293-5\_COPY\_1197\_1844  
Perfect score: 648  
Sequence: 1 ttcagagactgtctgaagt.....tgatccgaccagcagatttc 648

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gss1:  
9: gb\_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID      | Description        |
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| 1          | 646.4 | 99.8        | 1215   | 9 AY407058 | AY407058 Homo sapi |
| 2          | 646.4 | 99.8        | 2134   | 3 CR620685 | CR620685 full-leng |
| 3          | 635.4 | 98.1        | 2083   | 3 BC022490 | BC022490 Homo sapi |
| 4          | 592.8 | 91.5        | 1028   | 1 AL573084 | AL573084 AL573084  |
| 5          | 553.2 | 85.4        | 1213   | 9 AY407059 | AY407059 Pan trogl |
| 6          | 528   | 81.5        | 960    | 5 BX348832 | BX348832 BX348832  |
| 7          | 468.8 | 72.3        | 1218   | 9 AY407060 | AY407060 Mus muscu |
| 8          | 468.8 | 72.3        | 2443   | 3 AK048622 | AK048622 Mus muscu |
| 9          | 468.8 | 72.3        | 2475   | 3 AK019860 | AK019860 Mus muscu |
| 10         | 449.4 | 69.4        | 487    | 2 BF760470 | BF760470 PM4-CT064 |
| 11         | 442.6 | 68.3        | 758    | 7 CV116084 | CV116084 AGENCOURT |
| 12         | 389   | 60.0        | 823    | 7 CV078760 | CV078760 AGENCOURT |
| 13         | 370.8 | 57.2        | 652    | 7 CF951959 | CF951959 UT-M-HLO- |
| 14         | 353.8 | 54.6        | 597    | 7 CK903582 | CK903582 i660e09.Y |
| 15         | 347.2 | 53.6        | 353    | 1 AA253509 | AA253509 zt77c09.Y |
| 16         | 333.8 | 51.5        | 561    | 4 B1962885 | B1962885 i660e09.Y |
| 17         | 323.8 | 50.0        | 551    | 4 B1962932 | B1962932 i660e09.Y |
| 18         | 311.8 | 48.1        | 390    | 2 AW486232 | AW486232 71607 MAR |
| 19         | 304.6 | 47.0        | 1014   | 7 CN646781 | CN646781 ILLUMIGEN |
| 20         | 298.2 | 46.0        | 4257   | 3 AK088439 | AK088439 Mus muscu |
| 21         | 294.2 | 45.4        | 634    | 5 BP307288 | BP307288 BP307288  |
| 22         | 277.6 | 42.8        | 897    | 5 BU416193 | BU416193 603667484 |
| 23         | 273.2 | 42.2        | 800    | 5 BU171982 | BU171982 AGENCOURT |
| 24         | 272.2 | 42.0        | 603    | 7 CF169608 | CF169608 B0815H12- |

ALIGNMENTS

RESULT 1  
AY407058  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source  
gene  
ORIGIN  
Query Match  
Best Local Similarity  
Matches  
647; Conservative  
99.8%; Score 646.4; DB 9; Length 1215;  
Pred. No. 1.9e-182;  
Mismatches 1; Indels 0; Gaps 0;  
1 TTCAGAGACTGTCTGAAGTATTCAAATCAGGACACACCAATGCGCATCTCACCTTA 60  
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25 271.2 41.9 806 7 CK474660  
26 267.2 41.2 1056 5 BU131593  
27 264 40.7 825 7 CO398106  
28 256.2 39.5 866 7 CN972676  
29 249 38.4 579 1 AV749794  
30 249 38.4 647 5 BU451988  
31 245 37.8 717 7 CK959975  
32 241.6 37.3 902 5 B0892116  
33 239.4 36.9 721 6 CB528341  
34 234 36.1 702 6 CB461678  
35 231.8 35.8 735 1 AI862415  
36 229 35.3 438 1 AA125751  
37 223 34.4 890 5 BX734909  
38 221.2 34.1 715 5 BU284080  
39 218.2 33.7 574 7 CN983834  
40 216.4 33.4 811 7 CR446364  
41 207 31.9 851 7 CN956297  
42 202.2 31.2 445 7 CF529257  
43 202 31.2 650 7 CF529257  
44 194.2 30.0 372 7 CN954601  
45 185.6 28.6 752 7 CK484066

CK474660 AGENCOURT  
BU131593 603119087  
CO398106 AGENCOURT  
CN972676 20173\_124  
AV749794 AV749794  
BU451988 603772372  
CK959975 4101105\_B  
B0892116 AGENCOURT  
CB528341 UT-H-PT2-  
CB461678 721665\_MA  
AI862415 t016b10.x  
AA125751 2123401.r  
BX734909 BX734909  
BU284080 603865377  
CN983834 52535\_126  
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CF529257 UI-1-BC1p  
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CK484066 AGENCOURT

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QY 61 ACATTCCCTAAATTTCTACAGAAGAGATCAAGGGCTACTGTGCATGATGAAGCTGGAGGAGC 120
Db 625 ACATTCCCTAAATTTCTACAGAAGAGATCAAGGGCTACTGTGCATGATGAAGCTGGAGGAGC 684
QY 121 GGGTGACAAATTTATTCAGGACGCTGAGGATGGAGATGGCGTTGATTTTCAGAGGACTTGGAAA 180
Db 685 GGGTGACAAATTTATTCAGGACGCTGAGGATGGAGATGGCGTTGATTTTCAGAGGACTTGGAAA 744
QY 181 GAATATAAGTGGGATTTGGTAACCTTCAGGAGATATTTGGCTGGGAATGAGTTTGT 240
Db 745 GAATATAAGTGGGATTTGGTAACCTTCAGGAGATATTTGGCTGGGAATGAGTTTGT 804
QY 241 TCGCAACTGACTAATCAGCAAGCTGTATGCTTTAAATAACCTTAAAGACTTGGGAAGG 300
Db 805 TCGCAACTGACTAATCAGCAAGCTGTATGCTTTAAATAACCTTAAAGACTTGGGAAGG 864
QY 301 AATGAGGCTTACTCATTTGATGAAATTTCTATCTCTCAAGTGAAGAACTCAATATATAGG 360
Db 865 AATGAGGCTTACTCATTTGATGAAATTTCTATCTCTCAAGTGAAGAACTCAATATATAGG 924
QY 361 ATTCACTTTAAAGGACTTACAGGACAGCGCGCAAAATTAAGCAGCATCAGCCAAACGGA 420
Db 925 ATTCACTTTAAAGGACTTACAGGACAGCGCGCAAAATTAAGCAGCATCAGCCAAACGGA 984
QY 421 AATGATTTTATAGCACAAAGGATGAGACACGACAAATGATTTTGAATATGTTTCACAAAATG 480
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QY 481 CTAACAGGAGGCTGGTGGTTGATGATGATGCTGCTTCCAACTTGAACGGAATGACTAT 540
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QY 541 CCACAGAGGACGACACACAAATAGTTCAACGCGATTAATATGCTACTTGGAAAGGCTCA 600
Db 1105 CCACAGAGGACGACACACAAATAGTTCAACGCGATTAATATGCTACTTGGAAAGGCTCA 1164
QY 601 GGCTATTGCTCAAGGCCACCAACCATGATGATCCGACACGAGATTTC 648
Db 1165 GGCTATTGCTCAAGGCCACCAACCATGATGATCCGACACGAGATTTC 1212

RESULT 2
LOCUS CR620685
DEFINITION full-length cDNA clone CS0DI037YG20 of Placenta Cot 25-normalized
ACCESSION CR620685
VERSION CR620685.1 GI:50501492
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2134)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 2134)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Best Local Similarity 99.8%; Pred. No. 2.3e-182;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1190 ACATTCCCTAAATTTCTACAGAAGAGATCAAGGCTACTGTGCATGATGAAGCTGGAGGAGC 1249
QY 121 GGGTGACAAATTTATTCAGGACGCTGAGGATGGCGTTGATTTTCAGAGGACTTGGAAA 180
Db 1250 GGGTGACAAATTTATTCAGGACGCTGAGGATGGCGTTGATTTTCAGAGGACTTGGAAA 1309
QY 181 GAATATAAGTGGGATTTGGTAACCTTCAGGAGATATTTGGCTGGGAATGAGTTTGT 240
Db 1310 GAATATAAGTGGGATTTGGTAACCTTCAGGAGATATTTGGCTGGGAATGAGTTTGT 1369
QY 241 TCGCAACTGACTAATCAGCAAGCTGTATGCTTTAAATAACCTTAAAGACTTGGGAAGG 300
Db 1370 TCGCAACTGACTAATCAGCAAGCTGTATGCTTTAAATAACCTTAAAGACTTGGGAAGG 1429
QY 301 AATGAGGCTTACTCATTTGATGAAATTTCTATCTCTCAAGTGAAGAACTCAATATATAGG 360
Db 1430 AATGAGGCTTACTCATTTGATGAAATTTCTATCTCTCAAGTGAAGAACTCAATATATAGG 1489
QY 361 ATTCACTTTAAAGGACTTACAGGACAGCGCGCAAAATTAAGCAGCATCAGCCAAACGGA 420
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Db 1550 AATGATTTTATAGCACAAAGGATGAGACACGACAAATGATTTTGAATATGTTTCACAAAATG 1609
QY 481 CTAACAGGAGGCTGGTGGTTGATGATGCTGCTTCCAACTTGAACGGAATGACTAT 540
Db 1610 CTAACAGGAGGCTGGTGGTTGATGATGCTGCTTCCAACTTGAACGGAATGACTAT 1669
QY 541 CCACAGAGGACGACACACAAATAGTTCAACGCGCATTAATATGCTACTTGGAAAGGCTCA 600
Db 1670 CCACAGAGGACGACACACAAATAGTTCAACGCGCATTAATATGCTACTTGGAAAGGCTCA 1729
QY 601 GGCTATTGCTCAAGGCCACCAACCATGATGATCCGACACGAGATTTC 648
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RESULT 3
LOCUS BC022490
DEFINITION Homo sapiens cDNA clone IMAGE:4792831, containing frame-shift
errors.
ACCESSION BC022490
VERSION BC022490.1 GI:18490680
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2083)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
```



Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zebberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 2083)  
Director MGC Project.  
Direct Submission  
Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 32 Row: b Column: 11  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557314  
This clone has the following problem: frame shifted.

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Matches 647; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy 61 ACATTCCCTAATTTACAGAGAGATCAAGCCCTCTGTGCATGGAGCTGGAGGAGGC 120  
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Qy 121 GGGTGGCAATTATTTCAGCGCGTGGAGTGGCAGCGTTGATTTTCAGAGGACTTGGAAA 180

Db 1155 GGGTGGCAATTATTTCAGCGCGTGGAGTGGCAGCGTTGATTTTCAGAGGACTTGGAAA 1214  
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Db 1215 GAATATAAAGTGGGATTTGGTAAACCCCTTCAGGAGAAATATTGGCTGGGAATAGTTGTT 1274  
Qy 241 TCGCAACTGACTAATCAGCAAGCGTATGCTTAAATAACACCTTAAAGACTGGGAAGG 300  
Db 1275 TCGCAACTGACTAATCAGCAAGCGTATGCTTAAATAACACCTTAAAGACTGGGAAGG 1334  
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Qy 361 ATTCACTTTAAAGGACTTACAGGAGCAGCGCGCAAAATAAGCAGCATCAGCCAAACGGA 420  
Db 1395 ATTCACTTTAAAGGACTTACAGGAGCAGCGCGCAAAATAAGCAGCATCAGCCAAACGGA 1454  
Qy 421 AATGATTTAGCACAAAGGATGAGGACACAGCAAAATGATTTGCAAAATGTTCACAATG 480  
Db 1455 AATGATTTAGCACAAAGGATGAGGACACAGCAAAATGATTTGCAAAATGTTCACAATG 1514  
Qy 481 CTAACAGGAGGCTGGTGGTTTGATGCATGTGGTCTTCCAACTTGAACGGAATGTACTAT 540  
Db 1515 CTAACAGGAGGCTGGTGGTTTGATGCATGTGGTCTTCCAACTTGAACGGAATGTACTAT 1574  
Qy 541 CCACAGAG-GCAGAACACAAATAAGTTCAACGGCATTAAATGTTACTTCTGGAAGGCTC 599  
Db 1575 CCACAGAGGAGCAGACAAATAAGTTCAACGGCATTAAATGTTACTTCTGGAAGGCTC 1634  
Qy 600 AGCTATTGCTCAAGGCCAACCAACCATGATGATCCGACGAGATTTTC 648  
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RESULT 4  
AL573084/c  
LOCUS  
DEFINITION  
AL573084 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1037YG20 3-PRIME, mRNA sequence.  
AL573084 1028 bp mRNA linear EST 06-APR-2004  
AL573084 3 GI:46246304  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

On Feb 16, 2001 this sequence version replaced gi:31294447.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4496.r  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?s=CS0D1037BD10NPl&c=4496.r>.

Location/Qualifiers  
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FEATURES  
source

/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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| Best Local Similarity   |  | 14671302  |  |
| Matches 628; Conservative   |  | 2 (bases 1 to 1213)   |  |
| 1   |  | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,         |  |
| 1002  |  | Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,             |  |
| 61  |  | Adams, M.D., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,             |  |
| 946   |  | Direct Submission   |  |
| 121   |  | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,                |  |
| 886   |  | Rockville, MD 20850, USA  |  |
| 181   |  | This sequence was made by sequencing genomic exons and ordering             |  |
| 826   |  | them based on alignment.  |  |
| 241   |  | FEATURES  |  |
| 766   |  | Location/Qualifiers   |  |
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| 361   |  | /mol_type="genomic DNA"   |  |
| 646   |  | /db_xref="taxon:9598"   |  |
| 421   |  | <1..>1213   |  |
| 586   |  | /gene="ANGPT2"  |  |
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| 541   |  | Query Match   |  |
| 466   |  | Best Local Similarity   |  |
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| 406   |  | Matches 555; Conservative 0; Mismatches 3; Indels 0; Gaps 0;                |  |
| AY407059  |  | QY 91 GCCTACTGTGACATGGAAGCTGGAGGAGCGGGTGGACAATATTTCAGGAGCTGAGGAT 150        |  |
| Pan troglodytes   |  | Db 655 GCCTACTGTGACATGGAAGCTGGAGGAGCGGGTGGACAATATTTCAGGAGCTGAGGAT 714       |  |
| AY407059.1  |  | QY 151 GGCAGCGTTGATTTTTCAGAGGACTTGGAAAGAATAATAAAGTGGGATTTGGTAACCTTCA 210    |  |
| GI:39763030   |  | Db 715 GGCAGCGTTGATTTTTCAGAGGACTTGGAAAGAATAATAAAGTGGGATTTGGTAACCTTCA 774    |  |
| Pan troglodytes (chimpanzee)  |  | QY 211 GGAGAAATATGGCTGGGAAATGAGTTTGTTCGCAACTGACTAATACGCAACGCTATGTTG 270     |  |
| Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;             |  | Db 775 GGAGAAATATGGCTGGGAAATGAGTTTGTTCGCAACTGACTAATACGCAACGCTATGTTG 834     |  |
| Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.          |  | QY 271 CTTAAATATACACCTTAAAGACTGGGAAGGAATGAGGCTTACTCATTCTATGTAACATTTTC 330   |  |
| Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., |  | Db 835 CTTAAATATACACCTTAAAGACTGGGAAGGAATGAGGCTTACTCATTCTATGTAACATTTTC 894   |  |
| Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,     |  | QY 331 TATCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAAAGGACTTACAGGGACAGCC 390    |  |
| Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,    |  | Db 895 TATCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAAAGGACTTACAGGGACAGCC 954    |  |
| Adams, M.D. and Cargill, M.   |  | QY 391 GGCAAAATTAAGCAGCATCAGCCCAACAGGAAATGATTTTAGCAACAAGGATGGAGACAAC 450    |  |
| Inferring nonneutral evolution from human-chimp-mouse orthologous   |  | Db 955 GGCAAAATTAAGCAGCATCAGCCCAACAGGAAATGATTTTAGCAACAAGGATGGAGACAAC 1014   |  |
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| clone CS0DI037YG20 5-PRIME, mRNA sequence.                          |  | Db 1015 GACAAATGTTTTCGCAATGTTTCAAAATGCTTAAACAGGAGCTGGTGGTTTGTATGTCATGT 1074 |  |
| clone CS0DI037YG20 5-PRIME, mRNA sequence.                          |  | QY 511 GGTCTCTTCCAACTTGAACCGAATGTACTATCCAGAGGCGAGAACACAAATTAAGTTCAAC 570    |  |
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| clone CS0DI037YG20 5-PRIME, mRNA sequence.                          |  | Db 1135 GGCATTAAATGGTACTACTGGAAAGGCTCAGGCTATTTCGCTCAAGGCCACAAACCATGATG 1194 |  |
| clone CS0DI037YG20 5-PRIME, mRNA sequence.                          |  | QY 631 ATCCGACCCAGCAGATTTTC 648   |  |
| clone CS0DI037YG20 5-PRIME, mRNA sequence.                          |  | Db 1195 ATCCGACCCAGCAGATTTTC 1212   |  |
| clone CS0DI037YG20 5-PRIME, mRNA sequence.                          |  | RESULT 6  |  |
| clone CS0DI037YG20 5-PRIME, mRNA sequence.                          |  | LOCUS   |  |
| clone CS0DI037YG20 5-PRIME, mRNA sequence.                          |  | BX348832  |  |
| clone CS0DI037YG20 5-PRIME, mRNA sequence.                          |  | DEFINITION  |  |
| clone CS0DI037YG20 5-PRIME, mRNA sequence.                          |  | BX348832 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA          |  |
| clone CS0DI037YG20 5-PRIME, mRNA sequence.                          |  | clone CS0DI037YG20 5-PRIME, mRNA sequence.                                  |  |

ACCESSION BX348832  
 VERSION GI:30365305  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 960)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4496.x  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?s=CS0BAG030ZC09\_CS02851\_1&c=4496.x

FEATURES  
 source Location/Qualifiers  
 1..960  
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 /clone="CS0D1037IG20"  
 /tissue\_types="PLACENTA COT 25-NORMALIZED"  
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 /notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
 Query Match 81.5%; Score 528; DB 5; Length 960;  
 Best Local Similarity 94.7%; Pred. No. 6.2e-147;  
 Matches 577; Conservative 0; Mismatches 28; Indels 4; Gaps 3;  
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 354 TTCAGAGACTGTGCTGAAGTATTCAAAATCAGGACACACCAATGGCATCTACACGTTA 413  
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 121 GGGTGGACAATTTACAGCGACGTGAGATGGCAGCGTTGATTTTCAGAGACTTGGAAA 180  
 474 GGGTGGACAATTTACAGCGACGTGAGATGGCAGCGTTGATTTTCAGAGACTTGGAAA 533  
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 361 ATTACCTTTAAGGACTTACAGGACACCGCGCAAAATTAAGCAGCATCAGCAACCAAGGA 420  
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 421 AATGATTTTACGACAAAGGATGGAGACAAACGACAAATGTTTTCAGAAATGTTTCAAAATG 480  
 773 AATGATTTTACGACAAAGGATGGAGACAAACGACAAATGTTTTCAGAAATGTTTCAAAATG 832

QY 481 CTAACAGGAGGCTGGT--GGTTTGATGATGTCGTCCTTCCAACCTTGAACGGAATGACT 538  
 DB 833 CTAACAGGAGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 892  
 QY 539 ATCCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 598  
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RESULT 7  
 AY407060 1218 bp DNA linear GSS 15-DEC-2003  
 LOCUS Mus musculus ANGPT2 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AY407060  
 VERSION AY407060.1 GI:39763031  
 SOURCE GSS.  
 KEYWORDS Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 1218)  
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1218)  
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
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 Best Local Similarity 82.7%; Pred. No. 4e-129;  
 Matches 536; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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 1 TTCAGAGACTGTGCTGAAGTATTCAAAATCAGGACACACCAATGGCATCTACACGTTA 60  
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 61 ACATTCCCTTAATTTACAGAGAGATCAAGCCCTACTGTGACATGGAGCTGGAGGAGGC 120  
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 121 GGGTGGACAATTTATTCAGCGACGCTGAGGATGGCAGCGTTGATTTTCAGAGACTTGGAAA 180  
 688 GGGTGGACAATTTATTCAGCGACGCTGAGGATGGCAGCGTTGATTTTCAGAGACTTGGAAA 747  
 181 GAATATAAGTGGAGTTGGTAAACCTTCAGGAGAAATATGGCTGGGAAATGAGTTGTT 240

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| Db         | 1048  | CTCTCAGGAGGCTGGTGTGTTGATGATGTCGTCCTTCCAACTTGACCGAATGTACTAT     | 1107            |
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| AK048622   |   |  |                 |
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| DEFINITION | Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30089A05 product:ANGIOPOIETIN-2 PRECURSOR, full insert sequence. |  | HTC 03-APR-2004 |
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| ORGANISM   | Mus musculus  |  |                 |
| REFERENCE  |   |  |                 |
| AUTHORS    | Carninci, P., and Hayashizaki, Y.   |  |                 |
| TITLE      | High-efficiency full-length cDNA cloning  |  |                 |
| JOURNAL    | Meth. Enzymol. 303, 19-44 (1999)  |  |                 |
| MEDLINE    | 99279253  |  |                 |
| PUBMED     | 10349636  |  |                 |
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| TITLE       | FANTOM Consortium.  |
| JOURNAL     | Functional annotation of a full-length mouse cDNA collection  |
| REFERENCE   | Nature 409, 685-690 (2001)  |
| AUTHORS     | 5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  |
| TITLE       | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  |
| JOURNAL     | Nature 420, 563-573 (2002)  |
| AUTHORS     | 6 (bases 1 to 2443)   |
| TITLE       | Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. |
| TITLE       | Direct Submission   |
| JOURNAL     | Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)  |
| COMMENT     | cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/ Location/Qualifiers   |
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| Query Match | 72.3%; Score 468.8; DB 3; Length 2443;  |

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| Best Local Similarity 82.7%; Pred. No. 5e-129;   |      |  |      |
| Matches 536; Conservative 0; Mismatches 112; Indels 0; Gaps 0;   |      |  |      |
| QY   | 1    | TTCCAGAGACTGTGCTGAAGTATTCAAAATCAGGACACACCAAAATGGCATCTTACACGTTA     | 60   |
| DB   | 1082 | TTCCAGAGACTGTGGGAAATCTTCAAGTCAGGACTCACACCAGTGGCATCTTACACACTG       | 1141 |
| QY   | 61   | ACATTCCTTAATTTCTACAGAGAGATCAAGGCTTACTGTGACATGAGAGCTGGAGAGGC        | 120  |
| DB   | 1142 | ACCTTTCCCAACTCCACAGAGAGATCAAGGCTTACTGTGACATGAGAGCTGGGTGGAGA        | 1201 |
| QY   | 121  | GGGTGGACAAATTTATTTTCAGCGAGCTGAGGATGCGAGGCTTGTATTTTTCAGAGGACTTCGAAA | 180  |
| DB   | 1202 | GGGTGGACAGTCATCCAACCCAGAGAGATGGCAGTGTGGACTTCCAGAGACCTGGGAA         | 1261 |
| QY   | 181  | GAATATAAGTGGGATTTGGTAAACCTTTCAGGAGAAATATTGGCTGGGAAATGAGTTTGT       | 240  |
| DB   | 1262 | GAATACAAAGAGGGCTTCGGAGGCCCTCTGGAGAGTACTGGCTGGCAATGAGTTTGTCT        | 1321 |
| QY   | 241  | TCGCAACTGACTAATCAGCAACGCTATGTGCTTTAAATAACACCTTAAAGACTGGGAAGG       | 300  |
| DB   | 1322 | TCCAGCTGACCGGTGAGCACCGCTACGTGCTTAAAGATCCAGCTGAAGGACTGGGAAGGC       | 1381 |
| QY   | 301  | AATGAGGCTTACTCATTTGATGATCAATTTCTCTCAAGTGAAGAACTCAATTTATAGG         | 360  |
| DB   | 1382 | AACGAGGCGCATTCGCTGTATGATCACTTCTACTGCTGGTGAAGAGTCCAACTACAGG         | 1441 |
| QY   | 361  | ATTCACTTTAAGGACTTACAGGAGACGCGGCAAAATAAGCAGCATCAGCCACACAGGA         | 420  |
| DB   | 1442 | ATTCACTTTACAGGACTCAGCGGACCGCGGCAAAATAAGTAGCATCAGCCACACAGGA         | 1501 |
| QY   | 421  | AATGATTTTACGCAAGGATGGAGACAAAGCAAAATGATTTTGCAAATGTTCAAAATG          | 480  |
| DB   | 1502 | AGTGATTTTACGCAAGGATTCGGAACAATGACAAATGCATCTGCAAGTGTTCAGATG          | 1561 |
| QY   | 481  | CTAACAGAGGCTGGTGGTTTGCATGATGCTGTCTTCCAACTTGAACGAAATGACTAT          | 540  |
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| QY   | 541  | CCACAGAGGCGAGAACACAAATTAAGTTCAACGGCATTAATGGTACTTCTGGAAGGCTCA       | 600  |
| DB   | 1622 | CCCAAAAACAGATACAAATAAGTTTAAACGGTATCAAGTGTGTTACTTCTGGAAGGGTCC       | 1681 |
| QY   | 601  | GGCTATTGCTCAAGGCCACACCATGATGATCCGACACGAGATTTTC                     | 648  |
| DB   | 1682 | GGCTACTGCTCAAGGCCACACCATGATGATCCGCGCCAGCAGATTTTC                   | 1729 |
| RESULT 9   |      |  |      |
| AK019860   |      |  |      |
| LOCUS  |      |  |      |
| DEFINITION   |      |  |      |
| Mus musculus 11 days pregnant adult female ovary and uterus cDNA,<br>RIKEN full-length enriched library, clone:5031400E18<br>Product:ANGIOPOIETIN-2 PRECURSOR, full insert sequence. |      |  |      |
| AK019860   |      |  |      |
| VERSION  |      |  |      |
| KEYWORDS   |      |  |      |
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| Mus musculus<br>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.                              |      |  |      |
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| MEDLINE  |      |  |      |
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| AUTHORS  |      |  |      |
| TITLE  |      |  |      |
| JOURNAL  |      |  |      |
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| AUTHORS  |      |  |      |
| TITLE  |      |  |      |
| JOURNAL  |      |  |      |
| MEDLINE  |      |  |      |
| PUBMED   |      |  |      |
| REFERENCE  |      |  |      |
| AUTHORS  |      |  |      |
| TITLE  |      |  |      |
| J  |      |  |      |

|            |  |  |                             |
|------------|--|--|-----------------------------|
| Db         | 1714   | GGCTACTCGCTCAAGCCCAACCATGATGATCGGCCAGACAGATTTC | 1761                        |
| RESULT 10  |  |  |                             |
| BF760470/c |  |  |                             |
| LOCUS      | BF760470   | 487 bp   | mRNA linear EST 12-JAN-2001 |
| DEFINITION | PM4-CT0641-211200-006-e08 CT0641   | Homo sapiens cDNA,                             | mRNA sequence.              |
| ACCESSION  | BF760470   |  |                             |
| VERSION    | BF760470.1   | GI:12108370                                    |                             |
| KEYWORDS   | EST.   |  |                             |
| SOURCE     | Homo sapiens (human)   |  |                             |
| ORGANISM   | Homo sapiens   |  |                             |
|            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |  |                             |
|            | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |  |                             |
| REFERENCE  | 1 (bases 1 to 487)   |  |                             |
| AUTHORS    | Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R.,<br>Ngaim, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,<br>Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,<br>Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,<br>O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and<br>Simpson, A.J. |  |                             |
| TITLE      | Shotgun sequencing of the human transcriptome with ORF expressed<br>sequence tags  |  |                             |
| JOURNAL    | Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)   |  |                             |
| MEDLINE    | 20202663   |  |                             |

|          |          |   |   |
|----------|----------|---|---|
| 02028663 | 10737800 | Contact: Simpson A.J.G.<br>Laboratory of Cancer Genetics<br>Ludwig Institute for Cancer Research<br>Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil<br>Tel: +55-11-2704922<br>Fax: +55-11-2707001<br>Email: asimpson@ludwig.org.br<br>This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL.<br>(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-CT0641-211200-006-e08&t3=2000-12-21&t4=1)<br>Seq primer: puc 18 forward<br>High quality sequence start: 19<br>High quality sequence stop: 487.<br>Location/Qualifiers<br>1..487<br>/organism="Homo sapiens"<br>/mol_type="mRNA"<br>/db_xref="taxon:9606"<br>/dev_stage="Adult"<br>/clone_lib="CT0641"<br>/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." | 69.4%; Score 449.4; DB 2; Length 487;<br>Best Local Similarity 98.7%; Pred. No. 2e-123;<br>Matches 453; Conservative 0; Mismatches 6; Indels 0; Gaps 0; |
| QY       | 87       | CAAGCGCTACTGTGATCGAAGCTGGAGGCGGGTGGACAAATTATTTCAGCGAGCTGA   | 146   |
| Db       | 484      | CACGTGCCAATTGTGATCGAAGCTGGAGGCGGGTGGACAAATTATTTCAGCGAGCTGA  | 425   |
| QY       | 147      | GGATGGCAGCGTTGATTTTTCAGAGCACTTGGAAAGAAATAAAGTGGGATTTGGTAACCC  | 206   |
| Db       | 424      | GGATGGCAGCGTTGATTTTCAGAGCACTTGGAAAGAAATAAAGTGGGATTTGGTAACCC   | 365   |
| QY       | 207      | TTTCAGAGAAATATTCGGCTGGGAAATGAGTTTGTTCGCAACTGACTAATCAGCAACGCTA   | 266   |
| Db       | 364      | TTTCAGAGAAATATTCGGCTGGGAAATGAGTTTGTTCGCAACTGACTAATCAGCAACGCTA   | 305   |



QY 267 TGTGCTTAAATACACCTTAAAGACTGGGAGGGAATGAGGCTTACTCATTTGTATGAACA 326  
Db 304 TGTGCTTAAATACACCTTAAAGACTGGGAGGGAATGAGGCTTACTCATTTGTATGAACA 245  
QY 327 TTTCTATCTCTCAAGTGAAGAACTCAATTATAGATTACCTTTAAAGGACTTACAGGGAC 386  
Db 244 TTTCTATCTCTCAAGTGAAGAACTCAATTATAGATTACCTTTAAAGGACTTACAGGGAC 185  
QY 387 AGCCGGCAAAATAGCAGCATCAGCCAAACAGGAATGATTTTATAGCAAAAGATGAGA 446  
Db 184 AGCCGGCAAAATAGCAGCATCAGCCAAACAGGAATGATTTTATAGCAAAAGATGAGA 125  
QY 447 CAACGCAAAATGATTTTGGCAATGTTTCAAAATGCTTAACAGGAGGCTGGTGGTTGATGC 506  
Db 124 CAACGCAAAATGATTTTGGCAATGTTTCAAAATGCTTAACAGGAGGCTGGTGGTTGATGC 65  
QY 507 ATGTGGTCTTCCAACTTGAACGAATGTACTATCCACA 545  
Db 64 ATGTGGTCTTCCAACTTGAACGAATGTACTATCCACA 26

## RESULT 11

CV116084 758 bp mRNA linear EST 30-AUG-2004  
LOCUS AGENCOURT 31522930 NIH\_MGC\_269 Rattus norvegicus cDNA clone  
DEFINITION IMAGE:7462299 5', mRNA sequence.

## ACCESSION

CV116084

## VERSION

CV116084.1 GI:51634565

## KEYWORDS

EST.

## SOURCE

Rattus norvegicus (Norway rat)

## ORGANISM

Rattus norvegicus

## REFERENCE

1. (bases 1 to 758)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)

Tissue Procurement: Dr. Josef Lazar, Dr. Howard J. Jacob, Medical

College of Wisconsin

<http://image.llnl.gov>

Plate: LLAM15735 Row: g Column: 01

High quality sequence stop: 594.

Location/Qualifiers

1. 758

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/db\_xref="taxon:10116"

/clones="IMAGE:7462299"

/tissue\_type="whole placenta, 2 pooled"

/lab\_host="DH10B Tona"

/clone\_lib="NIH MGC 269"

Site 2: NotI; Tissue was collected from two pooled

placentas from the 21st day of pregnancy. 1st strand cDNA

was primed with a Not I - oligo(dT) primer,

double-stranded cDNA was cloned into the Not I and EcoRV

sites of pExpress-1. Library was size-selected for >1.25

kb fragments for an average insert size of 2.05 kb. A

normalized version of this library is also available

(NIH MGC 270). Library was constructed by Open Biosystems

(Huntsville, AL). Note: this is a Mammalian Gene

Collection library"

## FEATURES

source

## ORIGIN

Query Match 68.3%; Score 442.6; DB 7; Length 758;  
Best Local Similarity 81.2%; Pred. No. 2.5e-121;  
Matches 514; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 16 GAAGTATTCAAATTCAGGACACACCAAAATGGCATCTACACGTTAAACATTCCTAAATCT 75  
Db 2 GAATCTTCAAGTCAGATCTCACCAAGTGGGATCTACAGCTGACCTTCCCACTCC 61  
QY 76 ACAGAAGAGATCAAGCCCTACTGTGACATGGAAAGCTGGAGGAGCGGGTGGCAAAATPAT 135  
Db 62 ACAGAGAGGTCAAGCCCTACTGTGACATGGGATCTACAGCTGACCTTCCCACTCC 121  
QY 136 CAGCGACGTGAGATGGGACGCTTGTATTTTTCAGAGGACTTGGAAAGATATAAAGTGGGA 195  
Db 122 CAACACCGGGAAGATGGGACGCTTGTATTTTTCAGAGGACTTGGAAAGATATAAAGTGGG 181  
QY 196 TTTGGTAAACCTTTCAGGAGAAATATGGCTGGGAAATGAGTTTTCGCAACTGACTAAT 255  
Db 182 TTGGGAGGCCCTCTGGGAGAGTATTTGGTGGGCAACGAGTTTGTCTCCGAGCTGACAGT 241  
QY 256 CAGCAACGCTTATGTCTTAAATACACCTTAAAGACTGGGAGGGAATGAGGCTTACTCA 315  
Db 242 GGSCATCGCTACGTCTGAGATCCAGCTGAAGACTGGGAGGAGGAGGACACTCT 301  
QY 316 TTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATATAGGATTTCACTTAAAGGA 375  
Db 302 CTGTATGACACTTCTACCTGTCCGGCGAGGAGTCCAACTACAGGATTTACCTTTACAGGA 361  
QY 376 CTTTACAGGACAGCGCGCAAAATTAAGCAGCATCAGCAACCCAGGAAATGATTTTAGCACA 435  
Db 362 CTCACAGGACAGCGCGGCAAAATCAGTAGCATCAGCCCAACAGGAAATGATTTTAGCACA 421  
QY 436 AAGGATGGGAGACAAACGACAAATGTATTTGCAAAATGTTTCAAAATGCTTAAACAGGAGGTG 495  
Db 422 AAGATTCGACAAATGACAAATGCACTGCAAGTGTTCAGAGTCTTCAAGAGGCTGG 481  
QY 496 TGGTTTGTATGATGTGTCTTCCAACTTGAACGGAATGATCTATTCACAGAGGAGCAAC 555  
Db 482 TGGTTGACGATGTGTCTTCCAACTTGAATGGACAGTACTACCCCAAAAGAGCAAT 541  
QY 556 ACAATAAGTTTCAACGCGCATTAATGGTACTACTTGGAAAGGCTCAGGCTATTCGCTCAAG 615  
Db 542 ACCAATAAGTTTCAACGCGTATCAAGTGTACTACTTGGAAAGGCTCAGGCTATTCGCTCAAG 601  
QY 616 GCCACAACCATGATGATCCGACAGCAGATTTTC 648  
Db 602 GCCACGACCATGATGATCCGCGCCAGCAGATTTTC 634

## RESULT 12

CV078760

LOCUS

DEFINITION

AGENCOURT 31478860 NIH\_MGC\_251 Rattus norvegicus cDNA clone

IMAGE:7386206 5', mRNA sequence.

CV078760

ACCESSION

CV078760.1 GI:51545791

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1. (bases 1 to 823)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)

Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin  
cDNA Library Preparation: Open Biosystems  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1553 row: p column: 12  
High quality sequence stop: 670.  
Location/Qualifiers  
1. .823  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="IMAGE:7386206"  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH MGC 251"  
/note="Organ: thymus; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; RNA obtained from testis tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:  
5'-pGACTAGTCTTAGATCGGAGCGCGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 1.6 kb. This primary library is normalized (non-normalized primary library is NIH MGC\_250) and was constructed by Open Biosystems. Note: this is a NIH\_MGC library"

FEATURES  
source

ORIGIN

Query Match 60.0%; Score 389; DB 7; Length 823;  
Best Local Similarity 81.1%; Pred. No. 3.2e-105;  
Matches 452; Conservative 0; Mismatches 105; Indels 0; Gaps 0;  
QY 92 CTTACTGTGACATGGAGCTGGAGGAGCGGGTGGACAAATTATTCAGCGACGTGAGGATG 151  
Db 1 CCTACTGTGACATGGAGCTGGAGGAGCGGGTGGACGGTGCATCCAAACCCGGGAAGATG 60  
QY 152 GCAGCGTTCATTTTCAGAGGACTTGGAAAGATATTAAGTGGGATTTGTGTAACCTTCAG 211  
Db 61 GCAGCGTTCATTTTCAGAGGACTTGGAAAGATATTAAGTGGGATTTGTGTAACCTTCAG 120  
QY 212 GAGAAATATGGCTGGGAAATGATTTGTTTCGCAACTGACTAATCAGCAACGCTATGTGC 271  
Db 121 GAGAGTATTTGGCTGGCAACGAGTTTGTCTCCAGCTGACCAAGTGGGCATCGTACGTGC 180  
QY 272 TTAATAATCACCTTAAAGACTGGGAAGGAATGAGGCTTACTCATTTGATGAAACATTTCT 331  
Db 181 TGAAGATCCAGCTGAAGGACTGGGAAGGCGAGGACACACTCTCTGTATGAGCACTTCT 240  
QY 332 ATCTCTCAAGTGAAGCACTCAATTAGGATTCACCTTAAAGGACTTACAGGACAGCGG 391  
Db 241 ACCTGTCCGGCGAGGAGTCAACTACAGGATTCACCTTACAGGACTCAGGACAGCGGG 300  
QY 392 GCAAAATAGCAGCATCAGCAACCAAGGAAATGATTTTAGCAAAAGGATGAGACAACG 451  
Db 301 GCAAAATAGTACATCAGCAACCAAGGAAATGATTTTAGCAAAAGGATTCGGAACATG 360  
QY 452 ACAATGATTTGCAAAATGTTTCAAAATGCTCAAAAGGAGGCTGGTGGTTGATGATGTG 511  
Db 361 ACAAAATGCAATCTGCAAGTGTTCACAGATGCTCACAGGAGGCTGGTGGTTCGACGATGTG 420  
QY 512 GTCCCTTCAACTTGAACGGAATGTACTATCCACAGGCGAGCAACAATAAGTTCAACG 571  
Db 421 GTCCCTTCAACTTGAATGACAGTACTATCCCAAAAGCAAGATACGAATAAGTTCAACG 480  
QY 572 GCATTAATATGTTACTCTGAAAGGCTCAGGCTATTTCGCTCAAGGCGCAACCAATCATGA 631  
Db 481 GTATCAAGTGGTACTCTGAAAGGGTCCGGTTACTTCGCTCAAGGCGCAACCAATCATGA 540  
QY 632 TCCGACGACGATTTTC 648  
|||||

Db 541 TCCGGCCAGCAGATTTTC 557

RESULT 13  
CF951959  
LOCUS

DEFINITION  
CF951959 652 bp mRNA linear EST 20-NOV-2003  
IMAGE:30634009 5', mRNA sequence.

ACCESSION  
CF951959  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 652)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Dr. James Lin University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
http://genome.uiowa.edu/distribution/mouseefl.html  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

Seq primer: pYX-5.

Location/Qualifiers  
1. .652  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="CS7BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30634009"  
/tissue\_type="Upper Head"  
/dev\_stage="9.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH\_BMAP\_HL0"  
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I;  
Site 2: Not I; The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is CGAAGTGAAT. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH)."

ORIGIN

Query Match 57.2%; Score 370.8; DB 7; Length 652;  
Best Local Similarity 81.6%; Pred. No. 8.7e-100;  
Matches 429; Conservative 0; Mismatches 97; Indels 0; Gaps 0;  
QY 87 CAAGGCCCTACTGTGACATGGGAAGCTGGAGGAGCGGGTGGACAAATTATTCAGCGACGTGA 146  
Db 127 CCAGGCCCTACTGTGACATGGAGCTGGGTGGAGGGGTGGACAGTCATCCACACCGAGA 186  
QY 147 GGATGGCAGCGTTGATTTTTCAGAGACTTTGGAAAGATATATAAGTGGGATTTGGTAACC 206  
Db 187 AGATGGCAGCTGGACTTCCAGAGGACCTGGAAAGATACAAAGAGGGCTTCGGGAGGCC 246  
QY 207 TTCAGGACAATATTGGCTGGGAAATAGTTTGTTCGCACTGACTAATCAGCAACGCTA 266  
Db 247 TCTGGGAGAGTACTGGCTGGGCAATAGTTTGTCTCCAGCTGACCGGTGACACCGCTA 306  
|||||

267 TGTGCTTAATAATACACTTAAAGACTGGGAAGGAATGAGGCTTACTCATTTGTATGACA 326  
Db CGTGCTTAAGATCCAGCTGAATGACTGGGAAGGCAACGAGGCGCATTCGCTGTATGATCA 366  
Qy TTCTTATCTCTCAAGTGAAGAACTCAATTATAGGATTCACCTTAAAGGACTTACAGGGAC 386  
Db CTCTTACTCTCGTGGTGAAGAGTCCAACTACAGGATTCACCTTACAGGACTTACAGGGAC 426  
Qy AGCCGGCAAAATAGCAGCATCAGCCAAACGAGAAATGATTTAGCAAAAGGATGAGA 446  
Db CGCGGGCAAAATAGTAGCATCAGCCAAACGAGGAAGTATTTAGCACAAAGGATTCGGA 486  
Qy CAACGACAATATTTGCAAAATGTTTCAAAATGCTTAAACAGGAGGCTGTGTTTATGTC 506  
Db CAATGACAATATGCTATGCAAGTGTTCCTCAGATGCTCTCAGGAGGCTGGTGGTTGACGC 546  
Qy ATGTGGTCTTCCAACTTTGAACGGAATGTACTTCCACAGAGGAGGAGCAACAAATAGTT 566  
Db ATGTGGTCTTCCAACTTTGAATGAGCAGTACTACTCCCAAAACAGAGATCAAAATAGTT 606  
Qy CAACGGCATTAATATGTTACTTCTGGAAGGCTCAGGCTATTCGCTC 612  
Db TAACGGTATCAAGTGTACTTCTGGAAGGCTCGGCTACTCGCTC 652

RESULT 14  
CK903582  
LOCUS  
DEFINITION  
is60809.y5 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens  
cDNA clone IMAGE:5671385 5' similar to TR:O15123 O15123  
ANGIOPOIETIN-2. ; mRNA sequence.  
CK903582  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 597)  
Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,  
Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,  
Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,  
McCann,R., Cole,R., Teagareishvili,R., Williams,T., Jackson,Y. and  
Bowers,Y.  
WashU-Harvard Pancreas EST Project  
Unpublished (2000)  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@biohp.harvard.edu  
This read is a 5' RESEQUENCE of a previously sequenced pancreas  
clone  
This read has been verified (found to hit its original self in the  
correct orientation)  
Seq primer: -40RP from Gibco.  
Location/Qualifiers  
1. 597  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5671385"  
/sex="Both"  
/tissue\_type="Islets of Langerhans"  
/dev\_stage="Adult"  
/lab\_host="DH10B"  
/clone\_lib="Melton Normalized Human Islet 4 N4-HIS 1"  
/notes="Organ: Pancreas; Vector: pSPORT1; Site: 1; Not 1;  
Site 2: Sal 1; Starting library constructed using  
SuperScript Plasmid Library kit (Life Technologies). cDNA

made by oligo-dT priming. Size-selected by column  
fractionation; average insert size 1.08 kb. Library was  
amplified once on solid support and plasmid DNA from  
library was prepared. The library DNA was normalized by  
method #4 from Bonaldo, Lennon, and Soares 1996 Genome  
Research 6:791-806; 0.5 microgram single-stranded library  
Plasmid DNA was mixed with 5 micrograms PCR product  
representing library inserts and hybridized to an EcoT of  
20. Single-stranded (unhybridized) plasmid were isolated  
by hydroxyapatite chromatography and used to make this  
library."

Query Match 54.6%; Score 353.8; DB 7; Length 597;  
Best Local Similarity 99.4%; Pred. No. 1.1e-94;  
Matches 355; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTCCAGAGACTGTGCTGAAGTATTCAAAATCAGGACACACCAATGCGCATCTACACGTTA 60  
Db 241 TTCCAGAGACTGTGCTGAAGTATTCAAAATCAGGACACACCAATGCGCATCTACACGTTA 300  
Qy 61 ACATTCCTTAATTTCTACAGAAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAGGAGGC 120  
Db 301 ACATTCCTTAATTTCTACAGAAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAGGAGGC 360  
Qy 121 GGGTGGACAATTAATTCAGCGACGCTGAGGATGGCAGCGTTCATTTTCAGAGACTTGGAAA 180  
Db 361 GGGTGGACAATTAATTCAGCGACGCTGAGGATGGCAGCGTTCATTTTCAGAGACTTGGAAA 420  
Qy 181 GAATATAAAGTGGATTTGGTAACCCCTTCAGGAGATATTTGGCTGGGAAATGAGTTGTT 240  
Db 421 GAATATAAAGTGGATTTGGTAACCCCTTCAGGAGATATTTGGCTGGGAAATGAGTTGTT 480  
Qy 241 TCGCACTGACTAATCAGCAACGCTATGCTCTTAAATAACACCTTAAAGACTGGGAAGGG 300  
Db 481 TCGCACTGACTAATCAGCAACGCTATGCTCTTAAATAACACCTTAAAGACTGGGAAGGG 540  
Qy 301 AATGAGCTTACTCATTTGTATGAACATTTCTATCTCTCAAGTGAAGACTCAATAT 357  
Db 541 AATGAGCTTACTCATTTGTATGAACATTTCTATCTCTCAAGTGAAGACTCAATAT 597

RESULT 15  
AA253509 353 bp mRNA linear EST 06-AUG-1997  
LOCUS  
DEFINITION  
z777c09.r1 Soares NhrMPu S1 Homo sapiens cDNA clone IMAGE:669424 5'  
similar to TR:G285989 G285989 ORF, COMPLETE CDS. ; mRNA sequence.  
AA253509  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 353)  
Hallier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,  
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,  
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,  
White,Y., Wylie,T., Waterston,R. and Wilson,R.  
WashU-Merck EST Project 1997  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Possible reversed clone: similarity on wrong strand  
Insert Length: 879 Std Error: 0.00  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 309.

FEATURES  
source

Location/Qualifiers  
1..353  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:5563391"  
/db\_xref="taxon:9606"  
/clone="IMAGE:669424"  
/tissue\_type="Pooled human melanocyte, fetal heart, and pregnant uterus"  
/lab\_host="DH10B"  
/clone\_lib="Soares NhMPu S1"  
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ORIGIN

Query Match 53.6%; Score 347.2; DB 1; Length 353;  
Best Local Similarity 99.1%; Pred. No. 8.7e-93;  
Matches 349; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 281 ACCTTAAGACTGGGAGGGAATGAGGCTTATCTTATGATGACATTTCTATCTCTCAA 340  
Db 1 ACCTTAAGACTCGGAGGGGAATGAGGCTTATCTTATGATGACATTTCTATCTCTCAA 60  
QY 341 GTGAAGAATCAATTATAGGATTCACCTTAAAGGACTTACAGGCAGCGGCAAAATAA 400  
Db 61 GTGAAGAATCAATTATAGGATTCACCTTAAAGGACTTACAGGCAGCGGCAAAATAA 120  
QY 401 GCAGCATCAGCCCAACAGGAATGATTTTAGCACAAAGGATCGAGACAAAGCAATGTA 460  
Db 121 GCAGCATCAGCCCAACAGGAATGATTTTAGCACAAAGGATCGAGACAAAGCAATGTA 180  
QY 461 TTTGCAATGTTCAAAATGCTAACAGGAGGCTGGTGGTTGATGCATGGTCTCTTCCA 520  
Db 181 TTTGCAATGTTCAAAATGCTAACAGGAGGCTGGTGGTTGATGCATGGTCTCTTCCA 240  
QY 521 ACTTGAA CGGAATGTACTATCCACAGAGCGAGAACACAAATAAGTTCAACGGCATTAAAT 580  
Db 241 ACTTGAA CGGAATGTACTATCCACAGAGCGAGAACACAAATAAGTTCAACGGCATTAAAT 300  
QY 581 GGTACTACTGGAAAGGCTCAGGCTATTTCGCTCAAGGCCCAACCCATGATGAT 632  
Db 301 GGTACTACTGGAAAGGCTCAGGCTATTTCGCTCAAGGCCCAACCCATGATGAT 352

Search completed: July 29, 2005, 09:49:54  
Job time : 2294.57 secs